

# STIC Search Report

Biotech-Chem Library

#### STIC Database Tracking Number: 126127

TO: Dave Nguyen

Location: REM-2D31/2C18

Art Unit: 1632

Friday, July 02, 2004

Case Serial Number: 10/068160

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1A69

Phone: 571-272-2518 /80/8

barbara.obryen@uspto.gov

### **Search Notes**

Ex. Maugen, Part I of your search could only be done in the Registry file, Results are expensive to display there, so I pulled out the GenBounk hits & printed those records stip directly from GenBank, The Gen Bank printouts are schind the STN printouts. Please let me know if you have any questions. Barb





### STIC SEARCH RESULTS FEEDBACK FORM

### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

/ol	untary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
<b>A</b>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability)
	Results were not useful in determining patentability or understanding the invention.
Co	mments:

Drop off or send completed forms to STIC-Biotech-Chem Library/Remsen Bldg.



us-10-068-160-20.rnpb

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2, 2004, 08:11:05 ; Search time 138.732 Seconds (without alignments) 625.926 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
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/ cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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/cgn2 6/ptodata/2/pubpna/US60 NEW PUB.seq:*
/cgn2 6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3163042 seqs, 2412103800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 20, Appl	Sequence 8, Appli	79,		Sequence 7, Appli	Sequence 40, Appl	Sequence 81, Appl	Sequence 82, Appl	Sequence 4, Appli	Sequence 16, Appl	Sequence 1, Appli	Sequence 199, App	Sequence 99, Appl	Sequence 75, Appl
ID	US-10-068-160-20	US-10-666-022-8	US-10-194-035-79	US-10-068-160-16	US-10-068-160-7	US-10-194-035-40	US-10-194-035-81	US-10-194-035-82	US-10-666-022-4	US-10-666-022-16	US-09-960-631A-1	US-09-822-830A-199	US-10-416-314-99	US-10-194-035-75
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% Query Match	100.0	100.0	94.4	91.1	91.1	91.1	91.1	91.3	91.1	91.1	88.9	88.9	88.9	85.6
Score	18	18	17	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16	16	16	15.4
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Sequence 83, Appl Sequence 125602, Sequence 82230, A Sequence 7185, Ap	Sequence 97884, A Sequence 10345, A Sequence 14876, A Sequence 27811, A	114523, 114523, 98704, 32802, 45745,	9020 9020 9020 2666 13, 9, 412,	Sequence 1, Appli Sequence 513, App Sequence 513, App Sequence 13, App Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl
US-10-194-035-83 US-10-424-599-125602 US-10-424-599-8230 US-09-974-300-7185	US-10-424-599-97884 US-10-437-963-10345 US-10-437-963-14876 US-10-282-122A-27811	10-027-632- 10-027-632- 10-437-963- 10-369-493- 10-437-963-	US-10-437- US-10-437- US-10-437- US-10-260- US-10-349- US-10-156- US-10-156-	US-10-156-761-11 US-09-874-991C-513 US-09-874-991C-513 US-09-874-991C-513 US-10-068-160-12 US-10-068-160-13 US-10-068-160-14 US-10-068-160-14 US-10-068-160-14 US-10-068-160-14 US-10-068-160-14 US-10-068-160-14
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## ALIGNMENTS

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US-10-068-160-20

US-10-068-160-20

Sequence 20, Application US/10068160

PUBLICATION NO. US20030060440A1

GENERAL INCOMMUTION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SERVERLY, Deniela

APPLICANT: USRTHERY, Deniela

APPLICANT: USRTHERY, Deniela

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN INMUNE RESPONSE

FILE REFERENCE: 4239-64399

CURREAN FILING DATE: 2002-02-06

PRIOR PLIANG DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOOFWARE: PACENTING ONES: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 20

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

COTHER INFORMATION: Oligonucleotide

US-10-068-160-20

Query Match

Best Local Similarity 100.0%; Pred: No. 40;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTORICAND OF CONSERVACION OF CONSERVACION OF CONSERVACION OF MISMATCHES 0; INDELS OF CONSERVACION OF MISMATCHES 0; INDELS OF CONSERVACION OF CONSERVACION OF MISMATCHES 0; INDELS OF CONSERVACION OF C
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RESULT 2 US-10-666-022-8

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US-10-068-160-16

Sequence 16, Application US/10068160

Sequence 16, Application US/10068160

Publication No. US20030060440a1

GENERAL INFORMATION:

APPLICANT: THE COVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: TLINMAN, Dennis

APPLICANT: KLINMAN, Dennis

APPLICANT: KLINMAN, Dennis

APPLICANT: VERTHELYI, Daniela

ITTLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

CURRENT APPLICANTION NUMBER: US/10/068,160

CURRENT APPLICATION NUMBER: 60/128,898

PRIOR PELLING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOFTWARE PALENCE PALENCE IN VERSION 3.1

LENGTH: 18
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Publication No. US20030060440A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINAM, Dennis
APPLICANT: KLINAM, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE TILE REPERRENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT PAPLICATION NUMBER: 60/128,898
PRIOR PRILING DATE: 1999-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide US-10-068-160-16
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, OTHER INFORMATION: Oligonucleotide
US-10-068-160-7
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SOFTWARE: Patentin version 3.1
SEQ ID NO LENGTH: 20
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ORGANISM: Artificial Sequence
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Matches 17; Conservative
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Best Local Similarity 94.4*
Matches 17; Conservative
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US-10-194-035-40
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US-10-194-035-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1).7(20)
CTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-8
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Sequence 8, Application US/10666022
Publication No. US20040105872A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic
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Sequence 4, Application US/10666022;
Sequence 4, Application US/10666022;
Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services
APPLICANT: Wilman, Dennis M.
APPLICANT: Verthely: Daniela
APPLICANT: Verthely: Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS:
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS:
TITLE OF APPLICANTON NUMBER: US 66902
CURRENT APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 20
                                              Sequence 82, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL APPLICANT: THE GOVERNMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINAMA, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: USRTHELYI, Daniela
ITHE OF INVENTION: OLIGODEOXYNUCLECTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82
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NAME/KEY: misc feature
LOCATION: (1).7(20)
CTER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4; DB 15;
Pred. No. 2.3e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                      FILE REFERENCE: 4239-6337
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
FRIOR APPLICATION NUMBER: PCT/US01/01122
FRIOR FILING DATE: 2001-07-19
FRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 119
SOFWARE: Patentin Ver. 2.1
SEQ ID NO SEQ ID NOS: 120
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGTCGGTGCAGGGGG
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                          US-10-194-035-82
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Sequence 40, Application US/10194035

Publication No. US20030144229A1
GENERAL INPORMATION.
GENERAL INPORMATION.
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: KLINARN, Dennis
APPLICANT: KLINARN, Dennis
APPLICANT: KLINARN, Dennis
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TITLE REPRENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
SOFTWARE: PATENTING NUMBER: US 60/176,115
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR PATENT DATE: 2001-07-19
SOFTWARE: PATENT DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 81, Application US/10194035
Publication No. US2003014422941
GENERAL INFORMATION NO. US2003014422941
GENERAL INFORMATION
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: USERTHELYI, Daniela
TITLE OF INFERTION: OLIGOBOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
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JOTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40
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US-10-194-035-81
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Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1;
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Pred. No. 2.3e+02;
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CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
PRIOR PELLOR ON NUMBER: PT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 94.4%;
Matches 17; Conservative
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LENGTH: 20
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APPLICANT: AGOSTLIC,
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulveta, Kamalakar
APPLICANT: Graham, James R.
ITLE OP INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILLE REPERENCE: Gl. 6402.
FILLE REPERENCE: Gl. 6402.
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILLING DATE: 2001-03-29
FRIOR PILLING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SSOTHARE: Patent In Ver. 2.0
EBNGTH: 1192
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Pred. No. 1.9e+02;
0; Mismatches 0; Indels
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ING DATE: 2003-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/247,505
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/249,642
PRIOR FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWARNAKAR, Anita
CHAMLA, Nazinder K.
SANJANWALA, Madhusudan M.
THORNTON, Michael B.
ELLIOTT, Vicki S.
LU, Yan
GIETZEN, Kimberly J.
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APPLICANT: KAREHT, Stephanie K.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-0287 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Sco.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99, Application US/10416314 Publication No. US20040082508A1 GENERAL INFORMATION:
Senetics Institute, Inc. Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUNG, Li
HAFALIA, April J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HONCHBLL, Cynthia D.
LU, Dyung Aina M.
THANGAVELU, Kavitha
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APPLICANT: YAO, Monique G.
APPLICANT: GANDHI, Ameena R.
APPLICANT: BAUGEN, Mariah R.
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Best Local Similarity 100.0
Matches 16; Conservative
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XU, Yuming
YANG, Junming
LAL, Preeti G.
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ISON, Craig H.
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BANDMAN,
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                                                              Publication No. US20040105872A1

Publication No. US20040105872A1

Sequence 16, Application US/10666022

Publication No. US20040105872A1

SECRETARY INCOMMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Klinman, Dennis M.

APPLICANT: Klinman, Dennis M.

APPLICANT: Wetthely, Daniela

TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

CURRENT PLING DATE: 2003-09-17

PRIOR FILING DATE: 2003-09-18

NUMBER OF SEQ ID NOS: 181

SEQ ID NO 16

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Sequence 1, Application US/09960631A
Sequence 1, Application US/09960631A
Sequence 1, Application US/09960631A
APPLICANT: MINOCHNITCHENKO, Oleg
APPLICANT: WEI, Jiang
APPLICANT: NOUYE, Masayori
TITLE OF INVENTION: SOLUBLE ISCHEMIA ACTIVATED PROTEIN
FILE REPERBACE: 266/171
CURRENT APPLICATION NUMBER: US/09/960,631A
CURRENT FILING DATE: 2001.09-20
PRIOR PILLING DATE: 2000.09-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE PAREIN VERSION 3.1
SEQ ID NO 1
LENGTH: 840
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; Sequence 199, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
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100.0%; Fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                    US-10-666-022-16
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ઠે 쉽 RESULT 12

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APPLICANT: ISHLI, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTUON: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN INMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT PELLING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2000-01-14
SEQ ID NOS: 119
SCOFTWARE: Patentin Ver. 2.1
SEQ ID NO 83
FINAL PARTICAL ORDS SECOND SE
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Job time : 143.732 secs
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ORGANISM: Artificial Sequence
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Publication No. US2003014429A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: KILINGAN, Dennis
APPLICANT: VERTHELYI, Daniela
APPLICANT: VERTHELYI, Daniela
APPLICANT: USRTHELYI, Daniela
APPLICANT: USRTHELYI, Daniela
APPLICANT: VERTHELYI, Daniela
APPLICANTON ONUMBER: US/10/194,035
CURRENY APPLICATION NUMBER: PCT/US01/01122
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 75
LENGTH. 19
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US-10-194-015-83
US-10-194-015-83
US-10-194-015-83
Sequence 83, Application US/10194035
Publication No. US20020144229A1
GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-75
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Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1545079CB1
US-10-416-314-99
PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-21
PRIOR PLING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/254,305
PRIOR APPLICATION NUMBER: US 60/256,448
PRIOR APPLICATION NUMBER: US 60/256,448
PRIOR FILING DATE: 2000-12-18
NUMBER OF EGO ID NOS: 130
SOFTWARE: PERL PROGram
SEQ ID NO 99
IENGTH: 2487
TYPE: DNA
PRIOR HOMO SADIENS
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ORGANISM: Artificial Sequence
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US-10-194-035-75
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score:

Title: Perfect

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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AW325275 1-SEP-200
RNA linear EST 21-SEP-200
RNA Library Trypanosoma
cruzi cDNA clone 25h9 5', mRNA sequence.
AW325275
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
I (bases 1 to 245)
Porcel, B.M., Tran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,
Urmenyi, T.P., Rondinelli, E., Pettersson, U., Andersson, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Confact: Aslund L
Department of Medical Genetics
Uppsala University
Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
Tel: 46 18 471 45 85
Fax: 46 18 52 68 49
Email: lena.aslund@medgen.uu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene survey of the pathogenic protozoan Trypanosoma
Genome Res. 10 (8), 1103-1107 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
BJ216073
AL897989
BJ28246
AG082246
AG121475
BG554593
BW0688740
BW792946
BW792949
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4.4.4.4.4.4.4.4
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CEL74729 tigr-gss-
AQ444154 GSSTC0207
AL898002 AL898002
                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                55026578
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                       27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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CE174729
AQ444154
AL898002
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Gapop 10.0 , Gapext 1.0
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18
1 tgcgtcggtgcagggggg 18
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Match
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EST 21-SEP-2000

cruzi

Score

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16.4 16.4 16.4

BI746584 SALK 0448
BG913279 G02811967
AG082246 Pan trog1
BM068740 iee8 co5.79
BM058266 ie92f10.79
BM058266 ie92f10.79
BM058266 ie92f10.87
BM010828 AGBNCOURT
C0284597 G02CN94TV
C0284597 G02CN94TV
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C0284597 G02CN94TV
C0316713 G02CN94TV
C0284593 G02CN94TV
C0284593 G02CN94TV
BM05820 AGBNCOURT
C0107371 AGBNCOURT
BM05820 AGBNCOURT
BM377620 BX377620
BM3577620 BX377620
BM551929 AGBNCOURT

GSS 09-JAN-2001

trypanosoma

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/cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/clone_lib="Trypanosoma cruzi random genomic library"
/clone="Vector: pBs(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
Hincil site of the vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL898002 AGC-egg Silurana tropicalis cDNA clone TEgg043g16 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aires, Argentina

Par: (54-11) 4580/7255/7

Fax: (54-11) 4752-9639

Email: dsanchez@iib.unsam.edu.ar

Exageneres were basecalled with phred and vector was masked with crosmatch (see http://genome.washington.edu). Sequences were then trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silurana tropicalis (western clawed frog)
Silurana tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ampbibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinee, Silurana.
                                                                                                                                                                                       Trypanosoma cruzi.
Sukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 27)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosom cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
                    AQ444154 SSTC0207 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G10L7, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 14, 2000 this sequence version replaced gi:9372108. Contact: Sanchez D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Instituto de Investigaciones Biotecnologicas (Univ. Nac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.4; DB 28;
Pred. No. 1.5e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma cruzi"
/mol_cype="genomic DNA"
/strain="CL-Brener"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5693"
/clone="G10L7"
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Class: shotgun.
Location/Qualifiers
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                                                                                                                           AQ444154.3 GI:10130745
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Best Local Similarity 94.4%;
Matches 17; Conservative
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AL898002
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TiGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 25-SEP-2003
                                                                                 /organism="Trypanosoma cruzi"
/organism="Trypanosoma cruzi"
/strain="Cl-Bermer"
/strain="Cl-Bermer"
/db_xref="taxon:5693"
/clone="25h9"
/clone="1b="T.cruzi epimastigote normalized cDNA Library"
/clone="DNA library constructed with oligo dt primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (Pharmacia)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Carnivora, Pissipedia, Canidae, Canis.
1 (bases 1 to 271)
Kirness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 bp DNA linear GSS 25-SEP-20 tigr-gss-dog-17000326716213 Dog Library Canis familiaris genomic, genial survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9615"
/db_xref="taxon:9615"
/clone lb="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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91.1%; Score 16.4; DB 10; Length 245;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0
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/organism="Canis familiaris"
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/strain="Standard Poodle"
Seg primer: T7 primer
High quality sequence stop: 245.
Location/Qualifiers
1...245
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Canis familiaris
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AL897989 421 bp mRNA linear EST 04-DEC-2003
AL897989 XGC-egg Silurana tropicalis cDNA clone TEgg043e14 5', mRNA
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Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE: ID: TEGG043e14.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
ECDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
BCORI-Not1 cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and Not1 at the 3' end.
Vector: pCS107; Site 1: ECORI, Site_2: Not1
Host: Escherichia coli XL1-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="egg" /lab_host="egg="regg" /lab_host="Escherichia coli Xil-blue" /clone_lib="XGC-egg"; /clone_lib="XGC-egg7; Site_l: EcoRI; Site_2: NotI; cDNA was Oligo dr primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
   /tissue type="spike at meiosis"
/dev_stage="?eekes' scale 9"
/clome_lib="Y. Ogihara unpublished cDNA library,
                                                                                                                                                                            Length 400;
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Hinxton, Cambridgeshire, CB10 1SA, UK
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                                                                                                                                                                                                                                                                                                             1 TGCGTCGGTGCAGGGGG 18
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Matches 17, Conservative
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AL897989
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Mriticum destivum

Mriticum destivum

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta: Magnollophyta; Liliopsida; Poales; Poaceae,

Spermatophyta: Magnollophyta; Liliopsida; Poales; Poaceae,

Dooideae, Triticae, Triticum.

Dooideae, Triticae, Triticum.

S Gylara,Y. and Murai,K.

Expressed genes in Triticum aestivum

Unpublished (2002)

Contact: Tadasu Shin-i

Contact: For Genetic Resource Information

National Institute of Genetics

Illi Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-55-81-6855

Fax: B1-559-81-6855

Fax: Location/Qualifiers

SS Location/Qualifiers
                                                                                                                                                                                          Hinakon, Cambridgeshire, CB10 1SA, UK
Bmail: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG043g16.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
BCORI-NotI cut CDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XII-blue.
Location/Qualifiers
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/lab_host="Bscherichia coli XL1-blue"
/lab_host="Bscherichia coli XL1-blue"
/clone lib="XGC-egg"
/note="Vector: pGS107; Site_1: EcoR1; Site_2: Not1; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoR1-Not1 cut cDNA was then ligated into pGS107 with
EcoR1 at the 5' end and Not1 at the 3' end"
   Taylor, R., Zorn, A.M. and Rogers, J. project 2001 (11_2003)
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Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Roge
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 16, 2002 this sequence version replaced gi:22950395.
Conteat: Taylor R.
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Pred. No. 1.5e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Silurana tropicalis"
/mol_trype="mkNa"
/db_xref="taxon:8364"
/clone="TEgg043g16"
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/db_xref="taxon:4565"
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/db_xref="taxon:9598"
/clone="PTB-079807.R"
                                                                                                                                                                                         1. .1018
/organism="Homo sapiens"
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R.Site 2 : SacI.
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1 Similarity 94.4%;
17; Conservative
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/db xref="taxon:3102"
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602811967P1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943992
5′, mRNA sequence.
BG913279
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                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viribiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viribiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 429)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1018)
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic survey sequence. BH746584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g42480. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                  BH746584.1 GI:18959699
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Homo sapiens
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Matches 17; Conservative
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DEFINITION
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tokoda, A., Taylor, T.D., Yada, T., Tokoda, A., Toyoda, A., Taylor, T.D., Yada, T., Tokoda, Y., Watanabe, H. and Sakaki, Y.
Tokodi, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
T-7-22 Subhiro-chou, Tsuruni-ku, Yokohama, Kanagawa 230-0045; Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG082246 1110 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-079B07.R, genomic survey sequence.
AG082246
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Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4943992"
/issue_type="anaplastic oligodendroglioma with lp/19q
loss"
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10888 row: e column: 17
High quality sequence stop: 472.
Location/Qualifiers
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BAC end sequences of Library PTB
Unpublished
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ORIGIN

ò g ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

DEFINITION

AG121475

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415 bp mRNA linear EST 12-MAR-2002 ie84c05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens EM068740
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 415)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradowhl, G., Clifton, S., Hillier, L., Marra, M., Orbe, D., Mylie, T., Martin, J., Bistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tasgareishvili, R., Endocrine, Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Bmail: dmeltom@blohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
                                                           Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                        1 (bases it o 1404)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, B. E., Hastings, M.,
Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: Shotgun.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

/ organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="laxon:287"
/db xref="taxon:287"
/clone="pacs1-60 4763"
/clone=lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun library."
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Other_ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                                                                                                                                        University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Ext: 2066857244
Fax: 2066857244
Email: craymond@u.washington.edu
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        GI:27162271
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           32554593.1
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                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes DNA, clone: PTB-130114.F, genomic survey sequence. AG121475. G1:16650640 GSS.
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Pujiyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Pujiyama,A., Hattori,M., and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi.Ru, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL:http://kgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clonse are derived from the chimpanzee BAC library FIB This BAC end
was generated during the R&D process and may have higher chance of
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pacs1-60 2763.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60 2763, genomic survey seguence.
BZ554593
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Ban troglodytes
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Pan.
                                                                                                                                                                Gabs
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BAC end sequences of Library PTB
Unpublished
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91.1%; Score 16.4; DB 29; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                           Length 1110;
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// Organism="Pan troglodytes"
// mol type="panomic DNA"
// mol type="panomic DNA"
// mol type="panomic DNA"
// mol type="panomic DNA"
// clone="prb-130114.F"
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                                                                                                                                                           Indels
                                                                                                     Score 16.4; DB 29;
Pred. No. 1.7e+04;
0; Mismatches 1;
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative 0
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DEFINITION

ACCESSION

RESULT 11

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Gaps

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21C Frontier Korean BST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
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/sex="F"
                                                                                                      'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Plate: 4 row: D column: 03
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Location/Qualifiers
                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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BM792946
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                                                                                                                                                                                                                                                                 /tissue type="Islets of Langerhans"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
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Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). CDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
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obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov High quality sequence stop: 413.
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Mashington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y. Cole, R., Tsagareishvili, R., Winpublished (2000)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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88.9%; Score 16; DB 12; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels
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Homo sapiens
                                                                                                                                                                                                                                                       /sex="Both"
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ORIGIN

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/tissue type="Islets of Langerhans"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
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/clone lib="Melton Normalized Human Islet 4 N4-HIS !"
/clone lib="Melton Normalized Function of Site 2: Sal !; Starting 1 library constructed using
SuperScript Plasmid Library kit [Life Technologies) CDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size ! OB kb Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make Ithis
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1 (Bases 1 to 490)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, Y.Y., Kim, J.W., Chu, W.Y., Kim, S., and Xim, Y.S., Kim, Y.S.
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K-EST0073583 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-4-D03
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consortium, for clone orders contact: info@image.llnl.gov
High.quality sequence stop: 429.
Location/Qualifiers
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Fax: +82-42-860-4409
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Site_2: Not!; The poly (A) + RNA was dephosphorylated with
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with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
iste by treatment of T4 RNA ligase and the first strand
CDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60mz. The CDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoSI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained CDNA vectors were used for transformation of
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Homo sapiens
Homo sapiens
Homo sapiens
Homo sapiens
Homosapiens
Homo
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                                                                                                                                                                                Anotes Titologan: Stomach, Vector: pT773-Pac, Site 1: EcoRI, Site 2: Not1; The S22SNU16 library was contributed by the Sacares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Screan Cell Line Bank (KCLB): SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res S0: 2773-2780."
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Contact: Kim Yes.

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

S2 Genu-dong Vuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4470

Email: yongsungsmail.kribb.re.kr

Plate: 7 row: H column: 11

High quality sequence stop: 519.
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88.9%; Score 16; DB 12; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels
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competent cells B. coli TopiOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 519; Best Local Similarity 100.0%; Pred. No. 2.2e+04; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: July 2, 2004, 13:33:13 Job time : 1350.14 secs

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Sequence 7532, Ap Sequence 7811, Ap Sequence 7811, Ap Sequence 7681, Ap Sequence 3, Appli Sequence 13, Appli Sequence 13, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 319, App Sequence 319, App Sequence 319, App Sequence 319, App Sequence 219, App Sequence 219, App Sequence 219, App Sequence 2524, App Sequence 2
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Sequence 40, Appl
Sequence 12753, A
Sequence 139, App
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139, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                             Run on:
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	PSEUDOMONAS	O; PSEUDOMONAS
1877, Ap 13029, A 61731, Ap 61731, Ap 2752, Ap 6374, Ap 137, Appl 37, Appl	<u>2</u> <sub>.</sub>	de
Sequence 1 Sequence 5 Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 1 Sequence 1 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 8 Sequence 8 Sequence 8	SEQUENCES RELATING AD THERAPEUTICS	Length 885; i Indels 0; G SEQUENCES RELATING ND THERAPEUTICS
US-09-252-991A-1877 US-09-252-991A-13029 US-09-252-991A-6031 US-09-489-039A-6773 US-09-489-039A-2752 US-09-252-991A-6137 US-09-252-991A-1836 US-08-252-991A-1836 US-08-252-991A-1836 US-08-252-991A-1836 US-08-252-991A-377 US-09-372-392-377 US-09-032-337-37 US-09-252-991A-88502 US-09-252-991A-88502	MENTS AMINO ACID AGNOSTICS A 991A 88	Query Match Best Local Similarity 94.14; Pred. No. 1.34-02; Matches 16; Conservative 0; Mismatches 1; I  Qy 2 GGCGGTGGTGGAGGGG 18  Qy 2 GGCGGTGGTGGAGGGG 826  RESULT 2 US-09-22-991A-7811 ; Sequence 7811, Application US/09252991A ; Patent No. 6551795 ; GRNEAL INPORMATION: NUCLEIC ACID AND AMINO ACID SEQUITITE OF INVENTION: 1996-02-18 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUITITE OF INVENTION NUMBER: US 60/074,788 ; PRICE REPRESENCE: 107196.136 ; CURRENT APPLICATION NUMBER: US 60/094,190 ; PRIOR FILING DATE: 1998-02-18 ; PRIOR FILING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 7811
44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1  US-09-252-991A-7532/C  US-09-252-991A-7532/C  Sequence 7532, Application US/09252991A  Patent No. 6551795  GENERAL INFORMATION:  APPLICANT: Marc J. Rubenfield et al.  TITLE OF INVENTION: NUCLEIC ACID AND.  TITLE OF INVENTION: AERUGINOSA FOR DI.  TITLE OF INVENTION: AERUGINOSA FOR DI.  TITLE OF INVENTION: 107196.136  CURRENT FILING DATE: 1999-02-18  PRIOR PELING DATE: 1998-02-18  PRIOR PILING DATE: 1998-02-18  PRIOR PILING DATE: 1998-02-18  PRIOR PILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-07-27  NUMBER OF SEQ ID NOS: 33142  SEQ ID NO 7532  LENGTH: 885  TYPE: DNA  ORGANISM: PSeudomonas aeruginosa  US-09-252-991A-7532	85.6%; 94.1%; rative  MAGGGGG 1  AGGGGGG 6  ARCGGGGG 6  Whenfield  NUCLEIC A  ARRUGING 199-02-136 1998-02-136 1998-07-18 1938-07-18 1938-07-18
666 666 666 666 666 666 666 666 666 66	ULT 1 09-252-991A-7532/c degener 7532, Application Underent No. 6551795 ENERAL INFORMATION: March 1711LE OF INVENTION: March 1711LE OF INVENTION: AGRUGIT FILE REPERENCE: 107196.136 CURRENT APPLICATION NUMBER: OF RICH PLING DATE: 1999-PRIOR APPLICATION NUMBER: PRIOR PLING DATE: 1999-OF PRIOR PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-07 PRIOR PLING DATE: 1998-07 PRIOR PLING DATE: 1998-07 PRIOR PLING DATE: 1998-07 PRIOR PLING DATE: 1998-07 PRIOR APPLICATION NUMBER: 1998-07	Heery Match Heat Local Similarity 94.18 Hatches 16, Conservative COGTCGGTCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	SULT 1 -09-252-991A-7532 Sequence 7532, Apparent No. 655179 GENERAL INFORMATI APPLICANT: MATCHILLE OF INVENTI TITLE OF INVENTI CURRENT FILING DAT PRIOR PELING	Query Match Best Local Si Matches 16, 2 2 2 2 2 4 2 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
0 00 0 0000000000000000000000000000000	RESULT 1 US-09-25; Sequent Sequent GENERAL GENERAL TITLE TITLE TITLE TITLE TITLE TITLE FILE FILE FILE FILE FILE FILE FILE FI	Query Best   Matche Qy Db Db 108-09-22 US-09-22

335 GCTTCGGTGCAGGGGG 351

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GENERAL INFORMATION:
APPLICANT: Bliot, Kathryn J.
APPLICANT: Bliot, Steven B.
APPLICANT: Bliot, Steven B.
APPLICANT: Harbold Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                   Sequence 7681, Application US/09252991A

Sequence 7681, Application US/09252991A

Ratent No. 6551795

GERERAL INFORMATION:

ITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING:

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING:

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING:

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 7681

LENGTH: 1794
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COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopyy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Datentin Release #1.0, Version #1.25
SOFTWARE: 100 NUMBER: US/08/496,855A
PRILNG DATE: 20-UN-1995
PRILNG DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Setdman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1;
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1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9369B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08496855A Patent No. 5801232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7681
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                                                                                 RESULT 5
US-09-252-991A-7681/c
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US,09/252,991A

CURRENT PILLING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-7

NUMBER OF SEQ ID NOS: 33142

EENGTH: 1242
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Patent No. 6610836
GENERAL INPORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4664

LENGTH: 1392
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, OTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-489-039A-4664
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                                                                         Ouery Match 85.6%; Score 15.4; DB 4; Best Local Similarity 94.1%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
85.6%; Score 15.4; DB 4;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1;
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94.1%; Pred. No. 1.3e+02;
7ative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 7949, Application US/09252991A Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 GCGGCGTGCAGGGGG 525
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 94.1
Matches 16, Conservative
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US-09-252-991A-7949
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US-09-489-039A-4664
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Gaps

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PCT-US91-02311-9
SEQUENCE 9, Application PC/TUS9102311
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Balis, Stephen B
APPLICANT: Brust, Paul
APPLICANT: Brust, Paul
APPLICANT: Akong, Michael
APPLICANT: Velicelebi, Gonul
TITLE OF INVENTION: Receptor Compositions and Methods Employing Same
TITLE OF INVENTION: Receptor Compositions and Methods Employing Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pitch, Even, Tabin & Flannery
STRBT: 135 S. LaSalle St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 83.3%; Score 15; DB 5; Length 1521; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                               Query Match

83.3%; Score 15; DB 2; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                         /note= "Human neuronal NAChR beta-2 cDNA shown as top sequence in Fig 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREFT: 135 C. CLIT.
CITY: Chicago
STATE: 113
COUNTRY: UGA
ZTP: 60603
COMPUTER: 1EM PC COMPAINE
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPAINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US91/02311
FTLING DATE: 19910403
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Peder, SCOCE B
REFERENCE/DOCKET NUMBER: 51247/PCT
TELEPHONE: 312-372-7842
INFORMATION POR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TEMPORMATION POR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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; Sequence 13, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
APPLICANT: Blliot, Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                      1192 degredendenden 1206
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; PEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1521
; OTHER INFORMATION: /note:
; OTHER INFORMATION: cDNA.;
US-07-938-154-9
                                                                                                                                                                                                                                                                                                                      2 GCGTCGGTGCAGGGG 16
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Sequence 9, Application US/07938154
; Sequence 9, Application US/07938154
; Patent No. 5981139;
GENERAL INFORMATION:
APPLICANT: Harpold, Michael M.
APPLICANT: Brust, Paul
APPLICANT: Brust, Paul
APPLICANT: Akong, Michael
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: ALOUE
MUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pretty Schroeder Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
STREET: CA Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                               FEATURE:
NAME/KRY: misc feature
NAME/KRY: misc feature
CCATION: 1.1521
OTHER INFORMATION: /note= "Human neuronal NAChR beta-2
OTHER INFORMATION: CDNA shown as top nucleotide sequence in US-08-496-855A-3
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.3%; Score 15; DB 1; Length 1521; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,154
FILING DATE: 30-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US91/02311
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1991
APPLICATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 941 9380
TTELEPAN: 619-546-9392
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TTELEPAN: 619-546-9392
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TTELEPAN: 619-546-9304
TTELEPAN: 619-546-9304
TTELEPAN: 619-546-9304
TTELEPAN: 619-546-9305
TTELEPAN: 619-546-9305
TTELEPAN: 619-546-9305
TTELEPAN: 619-546-9306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDDESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1192 GCGTCGGTGCAGGGG 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GOGTCGGTGCAGGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
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2e+02;
thes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
NAME/KEY: Coding Sequence
LOCATION: 265...1773
OTHER INFORMATION: beta2 human neuronal nicotinic
OTHER INFORMATION: acetylcholine receptor
NAME/KEY: 5. UTR
LOCATION: 1...264
OTHER INFORMATION:
  TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACI
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND M
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: June 7, 1996
CLASSIFICATION WHEER: 08/484,722
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DAIE: 06/07/95
ATTORNEY/AGENT INPORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION:
TELEPHONE: 619-238-0969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1444 GCGTCGGTGCAGGGG 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: 3'UTR
LOCATION: 1774...
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-660-451A-13
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
    APPLICANT: Ellis, Steven B.

JETLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTRAGONISTS FOR HUMAN NEGRONAL TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS: SADDRESSER: Brown, Martin, Haller & McClain STREET: 1660 Union Street CITY: San Diego
                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FLING DATE: 07-UN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: CDS

) LOCATION: 265..1773

GOTHER INFORMATION: /product= "BETA-2 SUBUNIT"

US-08-487-556-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 4.5

PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman: Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPAX: 619-238-0962
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.3%; Soc
Best Local Similarity 100.0%; P.
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 2448 base pairs
nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           both
                                                                                                                                                                                                                                                    USA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                    COUNTRY:
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US-08-660-451A-13
Sequence 13, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Blliott, Kathryn J.
APPLICANT: Harpold, Michael M.

1444 GCGTCGCTGCAGGGG 1458

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RESULT 13
US-084-67-574-9
US-084-67-574-9
Sequence 9, Application US/08467574
Fatent No. 6022704
GENERAL INFORMATION:
APPLICANT: Blics, Kathryn J.
APPLICANT: Blics, Steven B.
TITLE OF INVENTION: Michael M.
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Brown, Martin, Haller & McClaim
CORRESPONDENCE Brown, Martin, Haller & McClaim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 2; Length 2450;
Pred. No. 2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
                                 TILING DATE: 15-001-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-WAR-1993
AFTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: 619-546-939;
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: CA.
COUNTRY: USA
ZIP: 9101-926

ZIP: 92101-926

COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDIO
COMPUTER: IBM COMPALIDIO
COMPUTER: IBM COMPALIDIO
COMPUTER: IBM COMPALIDIO
COMPUTER: FASESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: June 5, 1995
CLASSIFICATION FORMER: US 08/028,031
FILING DATE: MARCH 8, 1993
ATTORNEY AGENT INFORMATION:
NAME: Seidman, Stephanie I
REGISTATION NUMBER: 33,779
REGISTATION NUMBER: 33,779
REGISTATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1446 GCGTCGGTGCAGGGG 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GCGTCGGTGCAGGGG 16
                                                                                                                                                                                                                                                                                                                       2450 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
; LOCATION: 267.1775
US-08-700-636-9
APPLICATION NUMBER:
FILING DATE: 16-JUL
                                                                                                                                                                                                                                                                                                                   LENGTH: 2450 base F
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                  both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.3%; Score 15; DB 2; Length 245
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
STRESSEE: 1660 Union Street
CITY: San Diego
                                                                          CITY: San Diego
CITY: San Diego
CITY: San Diego
COUNTR: CA
COUNTR: USA
ZIP: 92101-2926
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTEM: DOS
SOFTWARE: FASTEM: USO
FILING DATE: UNDE 5, 1995
CLASSIFICATION NUMBER: US 08/028,031
FILING DATE: MARCH 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: SOSIGNAN: STEPHANIC INTERNATION:
TELECOMMUTCATION INTERNATION:
TELECOMMUTCATION INTERNATION:
TELECOMMUTCATION INTERNATION:
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1446 GCGTCGGTGCAGGGG 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
, LOCATION: 267..1775
US-08-466-589-9
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA FEATURE:
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Gaps

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Gaps

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APPLICANT: Elliot, Kathryn J.
Ellis, Steven B.
Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
                                                            Length 2450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%; Score 15; DB 4; Length 2450;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,985
FILING DATE: 27-Jun-2001
PRIOR APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/465,589,
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/465,589,
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie 1
REFERENCE/DOCKET NUMBER: 23,779
REFERENCE/DOCKET NUMBER: 24735-9949B
                                                                Score 15; DB 4;
Pred. No. 2e+02;
                                        83.3%; Scor.
100.0%; Pred. No. ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-892-985-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09892985
Patent No. 6664375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-587-5360
                                                                                                                                                                                                                                                      1446 GCGTCGGTGCAGGGG 1460
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GCGTCGGTGCAGGGG 16
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STRANDEDNESS: both
                                                         Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-892-985-9
   US-09-217-345-9
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Patent No. 6303753

GENERAL INFORMATION:
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
TITLE OF INVENTION: HUMAN NETRONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                             Query Match 83.3%; Score 15; DB 3; Length 2450; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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REGISTRATION NUMBER: 33,779
REFERNCE/DOCKET NUMBER: 24735-9949B
TELECOMMINICATION INPORMATION:
TELEPHONE: 619-450-8400
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WEDIUM TYPE: Diskette
COMPUTER: IPM COMPACTIBLE
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COMPUTER: DISM COMPACTIBLE
COMPUTER: DESCRIPTION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
FILING DATE: 05-UN-95
FILING DATE: 06-UN-95
FILING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1446 GCGTCGCTGCAGGGG 1460
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                              LENGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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SEQUENCE CHARACTERISTICS
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LOCATION: 267..1775
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STRANDEDNESS: both
                                                                                                                  TOPOLOGY: both
MOLECULE TYPE: cDNA
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ZIP: 92037
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US-08-467-574-9
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1446 GCGTCGGTCCAGGGG 1460

Search completed: July 2, 2004, 13:37:54 Job tice: 29.2073 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	8	Acc48305 CpG oligo	Acc83123 D class C	Aac80659 Immunogen	Aas09629 Immunorea	Abk46507 Immunosti	Aac80662 Immunogen	Aac80661 Immunogen	Aac80620 Immunogen	Aas09631 Immunorea	Aas09590 Immunorea	Aas09632 Immunorea	Abk46510 Immunosti	Abk46468 Immunosti	Abk46509 Immunosti	Acc48298 CpG oligo	Acc48320 CpG oligo		Acc48306 CpG oligo		Acc48321 CpG oligo		Acc83117 D class C
SUMMARIES	ACC48318	ACC48305	ACC83123	AAC80659	AAS09629	ABK46507	AAC80662	AAC80661	AAC80620	AAS09631	AAS09590	AAS09632	ABK46510	ABK46468	ABK46509	ACC48298	ACC48320	ACC48312	ACC48306	ACC48319	ACC48321	ACC83125	ACC83117
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% Query Match	100.0	100.0	100.0	94.4	94.4	94.4	91.7	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1
Score	18	18	18	17	17	17	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
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SNTS snTs rapy; ss.  capy; ss.  tumor immunothe reat diseases sn precursor with ligodeoxynucleot ligodeoxynucleot ating dendritic sepecially a patraining 3	useful for ger responses, thus are useful for an infectious s action or to act
od a fire by a paper of the pap	otif. The method is u lenhancing T cell re- te denditic cells ar mmune response to an prevent future infec-
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Indels

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Mismatches

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Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide; tuberculosis; gytokine; leishmaniasis, AlDS-associated Kaposis e tumour; thyroid; cancer; allergy, eczeme; allergic rhinitis; coryza; hay fever; schiscosomiasis; interferon gamma; lupus erythematosus; antimicrobial; esthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis; cyg motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; ss.
                                                                                                                                                                                                  D class CpG ODN sequence useful for encapsulating in SSCL, DV51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2002; 2002WO-US024235.
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-2001; 2001US-0308283P.
25-JUL-2002; 2002US-00206407.
                           TGCGTCGGTGCAGGGGG
                                                                                                                      ACC83123 standard; DNA; 20
                                                                                                                                                                           (first entry)
 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gursel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-482260/45.
                                                                                                                                                                                                                                                                                                                                                                   WO2003040308-A2.
                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                          27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003.
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                                                                                                                                                ACC83123;
 Matches
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ACC83123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a D type CpG oligodeoxymucleotide that is an example of claimed D type oligodeoxymucleotides (see ACC48294) of the invention. Mature dendritic cells are obtained by contacting a dendritic cell precursor, such as a monocyte, with such an oligodeoxymucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune cells are to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to a cativate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to
                                                                                                                                                                                                                                                                                                            CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleoride.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
'note= "N is any base (especially G) or no base"
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/note= "N is any base (especially G) or no base"
                                                                                ö
                                                                                                                                                                                                                                                                                   CpG oligodeoxymucleotide used for dendritic cell maturation.
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                                                     7; Length 20;
                                                                               0; Indels
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Pred. No. 68;
                            Seguence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 BP; 1 A; 3 C; 11 G; 3 T; 0 U; 2 Other;
                                                   100.0%; Score 18; DB 100.0%; Pred. No. 68; ive 0; Mismatches
 be used to produce activated T lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 26; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produce activated T lymphocytes
                                                                                                         TGCGTCGGTGCAGGGGGG 18
                                                                                                                          3 TGCGTCGTGCAGGGGG 20
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                                                                                                                                                                                                     ACC48305 standard; DNA; 20
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                                                                Local Similarity 100.
ses 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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                                                                                                                                                                                                                                                           11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                 ACC48305;
                                                     Query Match
                                                                               Matches
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ACC48305
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Joshi BH,

Kawakami K,

Ishii KJ,

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The invention relates to sterically stabilised cationic liposomes (SSCL)
which comprises a cationic lipid, a co-lipid, stabilising agent and
encapsulating a K type oligodeoxynucleotide (DNN) including a CpG motif.

The invention is useful in pharmaceutical composition for impairing
crowth of a solid tumour cell (e.g. human tumour cell) bearing an
interleukin-13 receptor in a subject; for stimulating an immune response,
which is expression of a cytokine (e.g. interferon gamma), patricularly
immunotherapeutic response against tumours or stimulating an invitro
an in vitro immune cell, and for inducing an immune response against an
in vitro immune cell, and for inducing an immune response against an
in vitro immune cell, and for inducing an immune response against an
in vitro immune cell, and for inducing an immune response against an
in vitro immune cell, and for inducing an immune response against an
in vitro immune cell, and for inducing an immune response against an
interfectious agent e.g. virus, bacteria and fungus. It is also useful for
delivering oligodeoxynucleotides including a CpG motif in clinical
applications; for treating infectious diseases (e.g. tulazemia, malaria,
francisella, schistosociated Kaposi's tumour, thyroid cancer
etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
bronchial or allergic asthma, urticaria, food allergies), autofimmune
closs and including a clabetes, rheumatoid arthritis, lupus erythematosus and
multiple sclerosis) and psoriaess. The present sequence is a D class CpG
ODN potentially useful for encapsulating in SSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   Disclosure, Fig 10C; 110pp; English.
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Best Local Similarity 100.
Matches 18; Conservative
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100.0%; 100.0%;

Query Match Best Local Similarity

18

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Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:79.
 TGCGTCGGTGCAGGGGGG
            AAC80659 standard; DNA; 19
                   (first entry)
                    14-FEB-2001
                AAC80659;
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CpG oligodeoxynucleotide; unmethylated, antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; B-cell response; antibody production; immune response induction; vaccine; altergy; aethoma; infection; bacterial; virtal; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimatcrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss.

12-APR-2000; 2000WO-US009839. 99US-0128898P ISHII K. VERTHELYI D. (KLIN/) KLINMAN D. WO200061151-A2. 12-APR-1999; 19-0CT-2000. Synthetic.

Verthelyi Klinman D, Ishii K,

(ISHI/) (VERT/)

WPI; 2001-006880/01.

Novel oligonuclectides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 36; 46pp; English

The invention relates to novel immunogenic CpG oligodeoxynucleotides CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and Comprise one of the generic sequences 5'-NNY-20G-WNN-3' or 5'-KY-CpG-KY C-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant CC optionally have phosphorothioate linkages which make them more resistant CC complex comprising an oligonucleotide of the invention and a targetting agent, and a pharmaceutical composition comprising the oligonucleotide elivery complex. The oligonucleotide are able to induce either a cell-composition comprising the oligonucleotide of the sequence 5'-KY-CpG-KY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' coll-mediated response and dendritic cells), which then release cytokines, coll-mediated to induce an humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or meliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic

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conditions, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozal infections such as tuberculosis, AIDS, cleinhania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus exponse, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-canner conjuganties, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to a vaccine to the host. The present sequence represents an immunogenic CpG oligodeoxymucleotide of the invention
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Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Gaps ô Length 19; 0; Indels 94.4%; Score 17; DB 4; Le 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; larity 100.0%; P. Conservative 0; Query Match Best Local Similarity

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1 TGCGTCGGTGCAGGGGG 17 3 recercerecaeces

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RESULT 5

AAS09629 standard; DNA; 19 (first entry) 26-SEP-2001 AAS09629; AAS09629 

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Immunoreactive CpG sequence-containing oligonucleotide #79.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimanue disorder; infection; bio-warfare; vaccine; antiense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AlDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences

Claim 5; Page 40; 48pp; English.

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The

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mediated immune response, involving non-B cell activation, interferon gamma (IRN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system deficiency, infection or a symptom resulting from exposure to bic-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antiseanse therapy. The ODN are useful for treating preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines cand other atopic conditions, for improving the efficacy of vaccines and other atopic manana system deficiency virus (HIV) and malania, for treating immune system deficiency virus (HIV) and malania, for treating immune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisela, e.g. lupus cuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, useful for inducing an immune response, preferably a cell-Anthrax and Listeria

Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Gaps ö Score 17; DB 4; Length 19; Pred. No. 1.9e+02; 0; Mismatches 0; Indels 94.4%; Scc... 100.0%; Pre 17; Conservative Best Local Similarity Query Match Matches

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13 1 TGCGTCGGTGCAGGGG 17 3 Tecercestecheses ઠે 셤

RESULT 6 ABK46507

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Immunostimulatory unmethylated CpG oligodideoxymucleotide #97. ABK46507 standard; DNA; 19 (first entry) 05-JUN-2002 ABK46507; 

unmethylated CpG; oligdideoxymucleotide; ODN; virucide; vaccine;

Paramyxoviridae, F protein, respiratory syncytial virus, RSV, viral bronchiolitis, pneumonia, infectious pulmonary disease, bronchopulmonary dysplasia, congenital heart condition, ss.

Synthetic.

WO200211761-A2.

14-FEB-2002.

19-AUG-2001; 2001WO-US041633

10-AUG-2000; 2000US-0224011P. 01-SEP-2000; 2000US-0229307P.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Klinman DM Mond JJ, Prince G,

WPI; 2002-227118/28.

Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxymucleotides.

Claim 4; Page 9; 30pp; English

The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae P protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The

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vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory synchial virus (RSV), the primary cause of viral broncholitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premeture, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxymucleotide that can be used in the creation of
                                                                                                                            Gaps
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                                                                                                        94.4%; Score 17; DB 6; Length 19; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
                                                                                      Seguence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
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                                                                                                                                              1 TGCGTCGGTGCAGGGG
                                                                                                                                                                                                               AACB0662 standard; DNA; 20
                                                                                                                                                                                                                                                      (first entry)
                                                                                                               Similarity 100.
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                                                                     the vaccine
                                                                                                                                                                                                                                   AAC80662;
                                                                                                         Query Match
                                                                                                                    Local
                                                                                                                            Matches
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CpG oligodeoxynucleotide, unmethylated, antigen-presenting cell; immunogenic; cytokine release, natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response.

B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. 12-APR-2000; 2000WO-US009839. 99US-0128898P. WO200061151-A2. 12-APR-1999; 19-0CT-2000. Synthetic.

(ISHI/) ISHII K. (VERT/) VERTHELYI D. (KLIN/) KLINMAN D.

Verthelyi Klinman D, Ishii K,

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WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent. allergies,

Claim 4; Page 36; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNN-3' or 5'-RY-CpG-RY -3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targetting agent, and a pharmaceutical composition comprising the oligonucleotide

cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with coligonuclectides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response and those of the sequence 5'-RNT-CpG-RNN-3' cell-mediated response, and those of the sequence 5'-RNT-CpG-RNN-3' cell-mediated response, and those of the sequence 5'-RNT-CpG-RNNN-3' chain stration, the oligonucleotide acts on antigen-presenting cells administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, cleading to activation of natural killer (RK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immunosenic CpG oligonucleotide is administered either alone or or normalizating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infections agent. The allergic conditions which may be treated include eczena, allergic conditions, and the infections which may be treated include viral, conditions, and the infections which may be treated include viral, bacterial, tungal and protozoal infections such as tuberculosis, Alds, carbemarosus, rheumatoid arthritis and multiple sclerosis, a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare, and immunogenic CpG oligonucle phantism presuone is used in antisense therefore the antisense in the indication of an imminiary and protozoner. The induction of an imminiary and protozoner than anti-induced phanting and imminiary and symptoms resulting from exposure to an agent of biological warfare, and immunogenic CpG membrasioner is used in antisense the phantism of the indication of imminiary phantican phantican of an antisense the phantican of the phantican of an antisense the phantican of the phantican o immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligomuclectide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CPG oligodeoxynuclectide of the invention delivery c 

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match

91.1%; Score 16.4; DB 4; Length 20; 94.4%; Pred. No. 3.7e+02; ive 0; Mismatches 1; Indels 1 TGCGTCGGTGCAGGGGG 18 3 recercearecaeceee Local Similarity 94.4 Matches ઠે g

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Gaps ..

> AAC80661 standard; DNA; 20 BP. RESULT 8 AAC8066:

AAC80661; 

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; humoral response; cell-mediated immune response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; blological warfare agent; cytostatic; antiarthritic; antimiczobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antialergic antialergic protozoacide; tuberculostatic;

Synthetic.

WO200061151-A2.

19-0CT-2000.

12-APR-2000; 2000WO-US009839.

99US-0128898P. 12-APR-1999;

(KLIN/) KLINMAN D.

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The invention relates to novel immunogenic CpG oligodecxynuclectides (AAC80581-C80733). The oligonuclectide are at least 10 bases long and comprise one of the generic sequences 5-NMNN-CpG-WNN-3' or 5'-RY-CpG-RY comprise one of the generic sequences 5-NMNY-CpG-WNN-3' or 5'-RY-CpG-RY comprise one of the generic sequences 5-NMNY-CpG-WNN-3' or 5'-RY-CpG-RY comprise one of the propertional place them more resistant composition and a planamaceutical composition comprising the oligonuclectide of the invention and a targetting cagent, and a planamaceutical composition comprising the oligonuclectide of the invention and a targetting cagent, and a planamaceutical composition comprising the oligonuclectide of the sequence 5'-RY-CpG-RY-3' being able to induce a humoral [B-cell, antibody) response, with oligonuclectides of the sequence 5'-RY-CpG-RY-3' being able to induce a humoral response of the sequence 5'-RY-CpG-RY-3' being able to induce a humoral response. It is thought that after administration, the oligonuclectide acts on antigen-presenting calls (e.g., macrophages and dendritic cells), which then release cytokines, clearing to activation of matural killer (KR) cells. A cell-mediated or activation of an immune response is useful for treating, preventing or an induction of an immune response is useful for treating, preventing or an induction of an immune response is useful for treating, preventing or the allergic conditions which may be treated include eczena, allergic conditions which may be treated include eczena, allergic conditions, and the infections which may be treated include eczena, allergic thinitis, hayfever, urticatia, food allergies and other atopic cused in the treatment of an anticiminal may be treated include eczena, allergic conditions, and the infections which may be treated include eczena, allergic cused in the treatment of an anticiminal may be treated include eczena, allergic conditions and echiciminal may be activated in subscribed with immune spense is useful for treating may be a vecine of a v
                                                                                                                                                                   Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms
                                                                                                                                                                                          allergies, cancer, and autormment.
                                                                        Verthelyi D;
                                                                                                                                                                                                                                                                     Claim 4; Page 36; 46pp; English.
                                                                     Klinman D, Ishii K,
(ISHI/) ISHII K.
(VERI/) VERTHELYI D.
                                                                                                                       WPI; 2001-006880/01.
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Length 20; Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other; Score 16.4; DB 4; Pred. No. 3.7e+02; 0; Mismatches 1; 94.48; Query Match
Best Local Similarity 94.4
Matches 17; Conservative

lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxymucleotide of the invention

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Gaps

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1, Indels

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AAC80620 standard; DNA; 20 RESULT 9 AAC80620 ID AAC

AAC80620;

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; 

cell-mediated immune response; T-cell response; humoral response; becal response; antibody production; immune response induction, vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. immunogenic; cytokine release; natural killer cell; NK cell activation;

Synthetic.

#0200061151-A2.

19-0CT-2000

12-APR-2000; 2000WO-US009839.

99US-0128898P 12-APR-1999;

(KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERT/) VERTHBLYI D.

Klinman D, Ishii K,

Verthelyi D;

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodecxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-MNN-CpG-WNN-3' or 5'-RY-CpG-RY CC -3'. The central CpG motif is unmethylated, and the oligonucleotides of the invention also relates to an oligonucleotide delivery complex comprising the invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targetting adent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral fe-cell, antibody response, with oligonucleotides of the sequence 5'-MNN-CpG-WNN-3' being able to induce a humoral response. It is thought that after cell-mediated response, and those of the sequence 5'-MNN-CpG-WNN-3' being able to induce a humoral response. It is thought that after daministration, the oligonucleotide acts on antigen-presenting cells administration, the oligonucleotide acts on antigen-presenting cells.

CC de., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response is useful for treating, preventing or an immune response is useful for treating, preventing or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infections agent. The allergic conditions which may be treated include eczema, allergic conditions, hayfever, urticaria, food allergies and other atopic conditions and the infections which may be treated include eczema, allergic conditions, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include eczema alone or in combination with an auti-cancer or sesociated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic Cpd eliberatin phocytes ex vivo, producing activated lymphocytes which are then inistered to the host. The present sequence represents an immunogenic oligodeoxynucleotide of the invention mune response is used in antisense therapy and to improve the efficacy a vaccine. The oligonucleotide is preferably administered to lymphocytes administered

Seguence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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 Length 20;
Score 16.4; DB 4; Length 2
Pred. No. 3.7e+02;
); Mismatches 1; Indels
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                                          18
 91.1%;
                                                                3 TGCGTCGATGCAGGGGG
 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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AAS09631

AAS09631 standard; DNA; 20 BP

AAS09631;

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #81.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; herappeutic; alleary; asthma; cancer; autocimemune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; se.

Synthetic.

WO200151500-A1

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sedneuces

Claim 5; Page 40; 48pp; English.

AASO9551-AASO9662 represent cligodeoxynuclectides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The CoN are useful for inducing an immune response, preferably a cell-condition of a number sesponse, preferably a cell-condition of a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. solid tumnour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or used in antisense therapy. The ODN are useful for treating preventing copy. As a large creations, including eczema, allergic rhinitis or copyza, hay fever, bronchial asthma, unticarial (hives), food allergies and other atopic conditions, for immenodeficiency virus (HIV) and allarin for treating immune system deficiency virus (HIV) and copy in the immune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis,

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AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The CpG sequences is different from another of the multiple CpG sequences. The CpG sequences is different from another of the multiple CpG sequences. The CpG sequence involving an immune response, preferably a cell-cpG sequence involving non-B cell activation, interferon gamma (TRN-gamma) production or a humonral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune cayetem e.g. autoimmune disorder or an immune system deficiency, infection or a symptom remulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODM are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; interleukin-6 production; biterapputic; allergy; asthma; cancer; autoimmune disorder; intection; bio-warfare; vaccine; antiennse therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistcosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Boola; Anthrax; Listeria; ss.
tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
symproma resulting from exposure of bio-warfare agent, including Ebola,
Anthrax and Listeria
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                                                                                                                                Length 20;
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                                                                                                                                                                       1; Indels
                                                                                  Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                            Score 16.4; DB 4;
Pred. No. 3.7e+02;
0; Mismatches 1;
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94.48;
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                                                                                                                                                Local Similarie, ...
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AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cellmediated immune response, production and immune response interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukine production in a host, for treating, preventing or ameliocrating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection
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and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immundeficiency wirus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Prancisella, schistosomiasis, tuberculosis, acquired immundeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Sbola,
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                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoreactive CpG sequence-containing oligonucleotide #82.
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                                                                                                                                                                                     Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
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94.4%; Pred. No. 3.7e+02;
iive 0; Mismatches 1;
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Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

the vaccine

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or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus multiple sclerosis, infections including Francisella, solistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola,
                                                                                                                                                                                                                                                                                                                                                       Anthrax and Listeria
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Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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Score 16.4; DB 4; Length 20;
Pred. No. 3.7e+02;
0; Mismatches 1; Indels
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                                                            1 TGCGTCGGTGCAGGGGGG 18
                                                                                        3 recercearecadedee 20
Match 91.1%;
Local Similarity 94.4%;
es 17; Conservative (
   Query Match
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Gaps

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ABK46510 standard; DNA; 20 RESULT 13 ABK46510

ABX46510;

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(first entry) 05-JUN-2002

unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine; Immunostimulatory unmethylated CpG oligodideoxynucleotide #100.

Paramyxoviridae, F protein, respiratory syncytial virus, RSV, viral bronchiolitis, pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.

Synthetic

WO200211761-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US041633 10-AUG-2000; 2000US-0224011P.

01-SEP-2000; 2000US-0229307P.

(JACK+) JACKSON FOUND ADVANCEMENT MILITARY MED.

Mond JJ, Prince G,

WPI; 2002-227118/28.

Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.

Claim 4; Page 9; 30pp; English.

The invention describes a vaccine comprising one or more epitopes of a baramyxoviridae Protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodideoxynucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory symcytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that premeture, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxymucleotide that can be used in the creation of 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae P protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxymucleotides.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                         unmethylated CpG; oligdideoxymucleotide; ODN; virucide; vaccine; Paramyroviridee; F protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.
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                                                                                                                                                                                                                                                                                                     Immunostimulatory unmethylated CpG oligodideoxynucleotide #58.
91.1%; Score 16.4; DB 6; Length 20; 94.4%; Pred. No. 3.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 16.4; DB 6; Length 20; 94.4%; Pred. No. 3.7e+02; ive 0; Mismatches 1; Indels
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                                                                                                 3 TGCGTCGATGCAGGGGG 20
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                                                                      1 TGCGTCGGTGCAGGGGGG 18
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01-SEP-2000; 2000US-0229307P.
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                                                                                                                                                                                                  ABK46468 standard; DNA; 20
                                                                                                                                                                                                                                                                      (first entry)
                                      Conservative
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les 17; Conservative
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                 Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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   Query Match
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                      Local
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ABK46468
                                    Matches
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The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by quanthe linked by phosphate bond,-oligodideoxynucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. Rs vas been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.
                                                                                                                                                                                  unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine; Paramyvoviridae; P protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; corgenital heart condition; ss.
                                                                                                                                                Immunostimulatory unmethylated CpG oligodideoxynucleotide #99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mond JJ, Prince G, Klinman DM;
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                                  ABK46509 standard; DNA; 20 BP.
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                                                                                                            05-JUN-2002 (first entry)
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                                                                        ABK46509;
RESULT 15
ABK46509
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1 TGCGTCGGTGCAGGGGGG 18 3 TGCGTCGATGCAGGGGGG 20 à 쉽

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0; Gaps

Query Match
91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

2, 2004, 08:31:39 Search completed: July Job time: 135.89 secs

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July 2, 2004, 08:11:05 ; Search time 138.732 Seconds (without alignments) 625.926 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
                                                                                                                                         1 tgcatcgacgcagggggg 18
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Maximum DB seq length: 2000000000
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18
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Perfect score:
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                                             OM nucleic
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                                                                                                                                         Sequence:
                                                                                                                                                                                                   Searched:
                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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S US-10-068-160-14 3 US-09-874-991C-49	-09-874-991C-5	3 US-09-874-991C-53	US-09-874-991C-54 US-09-874-991C-55	US-10-068-160	US-10-068-160-	US-10-068-160-5	US-10-068-16	US-10-194-03	US-10-194-03	US-10-194-	US-10-194-03	_	US-10-194	US-10	US-10-194-035-7	US-10	US-10-666-	US-10-666-022	US-10-666-	US-09-874-991C-5	US-09-874-9	US-09-874-991C-	-09-874-991C-53	US-09-874-991C-51	13 US-09-874-991C-523
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# ALIGNMENTS

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US-10-068-160-19

SQUENCE 19, Application US/10068160

SQUENCE 19, Application US/10068160

SQUENCE AL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE SAPPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: STINMAN, Dennis

APPLICANT: STINMAN, Dennis

APPLICANT: STINMAN, Dennis

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

CURRENT APPLICATION NUMBER: 10/10/68,160

CURRENT FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 19

IENGTH: 18

TYPE: DNA

ORCANISM: Artificial Sequence

FEATURE:

ORCANISM: Artificial Sequence

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ORCANISM: Artificial Sequence

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Db 1 TGCATCGACGCAC

18

RESULT 2 US-09-874-991C-498

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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
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                                                                                    APPLICANT: RICHAL MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: INACHOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPERBNCE: 07797.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PATENT VET. 2.1
SEQ ID NO 98
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR APPLICATION NUMBER: 60/209,797
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 11;
.ive 0; Mismatches 0; Indels
Sequence 498, Application US/09874991C Publication No. US20040052763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-874-991C-509
; Sequence 509, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
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; Publication No. US20040052763A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGCATCGACGCAGGGGG 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
                                                                          APPLICANT: MOND, JAMES J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-874-991C-509
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US-09-874-991C-542
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ENGTH: 20
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APPLICANT: MOND, JAMES J.
APPLICANT: FLUCRA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
ITILE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINAM, Dennis
APPLICANT: KLINAM, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGOMEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REPERRACE: 4239-61999
CURRENT APPLICATION NUMBER: 60/128,898
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR APLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 35
LENGTH: 20
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APPLICANT: SECRETARY, Dennis
APPLICANT: KLINMAN, Dennis
APPLICANT: SHII, Ken
APPLICANT: VERTHELYI, Daniela
CURRENT APPLICATION UNMBER: 108/10/194,035
CURRENT APPLICATION UNMBER: 2002-07-12
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US-09-874-991C-542
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100.0%; Score 18; DE
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches
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                 CURRENT APPLICATION NUMBER: US/09/874,991C CURRENT FILING DATE: 2001-06-07 PRIOR APPLICATION NUMBER: 60/209,797 PRIOR FILING DATE: 2000-06-07 NUMBER OF SEQ ID NOS: 620 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 542 LENGTH: 20
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Publication No. US20030144229A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
07787.0042-0
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Best Local Similarity 100.
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US-10-068-160-35
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US-10-194-035-88
Sequence 88, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennie
APPLICANT: ISHLI, Ken
APPLICANT: USHTHENYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLECTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILLE REFREENCE: 429-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 531, Application US/09874991C

Fublication No. US20040052763A1

GENERAL INFORMATION:

APPLICANT: MOND, JAMES J.

APPLICANT: MOND, JAMES J.

APPLICANT: KLINMAN, DENNIS M.

TILE OF INVENTION: IMMUNOSTHULATORY RNA/DNA HYBRID MOLECULES
FILE REPREENCE: 07783 - 10042-0

CURRENT TRINGO BATE: 2001-06-07

PRIOR APPLICATION NUMBER: 60/209,797

PRIOR PILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 620

SOUTHARE: PATENTIN VENTION: 21

SEQ ID NO 531

LENGTH: 28
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100.0%; Pred. No. 11;
ive 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
     CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION UNBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 519
LENGTH: 28
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
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Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Alimen. Dennis M. APPLICANT: Alimen. Dennis M. APPLICANT: Alimen. Dennis M. APPLICANT: Werthely, Daniel W. SUBJECTS WITH IMMUNOSTIMULATORY CPG
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SOFTWARE PRIOR FILING DATE: 2002-09-18
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APPLICANT: FLONAN, DENNIS M.
TITLE OF INVENTION: INMUNSCRIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPERBACE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          idarity 100.0%; Score 18; DB 17; Length 20; idarity 100.0%; Pred. No. 11; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
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100.0%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/USO1/01122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 100
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TGCATCGACGCAGGGGG 20
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LOCATION: (1)..(20)
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Best Local Similarity
Matches 18; Conserv
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LENGTH: 20
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-88
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US-09-874-991C-503
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APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: KICHAEL
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT PILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 503
LENGTH: 18
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Publication No. US2040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: KLINAL, MICHAREL
APPLICANT: KLINAL, MICHAREL
APPLICANT: KLINAL, MICHAREL
APPLICANT: KLINAL, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPERENCE: 077987,00482-0
CURRENT APPLICATION NUMBER: US/09/874,991C
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37;
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91.1%; Score 16.4; D
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 503, Application US/09874991C Publication No. US20040052763A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 513
LENGTH: 18
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100.08; Pre
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                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.0
Matches 17; Conservative
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 88
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-09-874-991C-503
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APPLICANT: KLINMAN, Dennis
APPLICANT: ISHLI, Ken
APPLICANT: ISHLI, Ken
APPLICANT: ISHLI, Ken
APPLICANT: OF INTENTION DENNIS
TILLS OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT PILING DATE: 1002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-513
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Pred. No. 77;
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Pred. No. 77;
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Sequence 551, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
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, OTHER INFORMATION: Oligonucleotide
US-10-068-160-12
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ORGANISM: Artificial Sequence
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94.48;
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ORGANISM: Artificial Sequence
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SOFWARE: Patentin version 3.1
SEQ ID NO 12
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
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RESULT 15

US-10-068-160-14

i Sequence 14, Application US/10068160

publication No. US2030060440A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KILNMAN, Dennis
APPLICANT: KILNMAN, Dennis
APPLICANT: SECRETARY, DEPRETED BY THE
APPLICANT: SIGNATION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TITLE OF INVENTION NUMBER: US/10/068,160
CURRENT APPLICATION NUMBER: 06/120,66
PRIOR PULING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SEQ ID NOS: 120
SEQ ID NO 14
SEQ ID NO 14
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  0; Gaps
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  1; Indels
0; Mismatches
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ORGANISM: Artificial Sequence
PEATURE:
17; Conservative
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OM nucleic - nu	nucleic search, using sw model
Run on:	<pre>July 2, 2004, 07:36:05; Search time 633.732 Seconds (without alignments) 1231.080 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-10-068-160-20 18 1 tgcgtcggtgcaggggg 18
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 2000000000
Post-processing	<pre># Minimum Match 0*     Maximum Match 100*     Listing first 45 summaries</pre>
Database :	GenEmbl:*  11

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	4479	AX465429 Sequence	AXI94440 Sequence AX194481 Sequence	AX194482 Sequence	AX465390 Sequence	AX465431 Sequence AX465432 Sequence	AE008951 Agrobacte	AE007898 Agrobacte	Continuation (7 of	AC018659 Homo Bapi	ALYSYLLU Streptomy BC008984 Homo sari	AY286020 Homo sapi	AXI/Z561 HOMO SADI AY286019 Homo sapi	AC104336 Homo sapi	AC133710 Oryza sat algoga70 Human DNA	AC136491 Oryza sat	AC022557 Homo sapi	ALS13473 Homo sapi	BX323850 Danio rer	AX194475 Sequence ax194483 Sequence	AX465425 Sequence	AX465433 Sequence	AJ339016 Homo sapi	AJ330295 Homo sapi	ALSSESS HOMO SADI AX438770 Sequence	AJ338994 Homo sapi	AR387935 Sequence AK101989 Orvza sat	U39195 Human clone	36 Or		Methar	Vib	AEVV45/1 Pseudomon		DNA linear PAT 28-AUG-2001		5			induce an immune response h and Human Services (US)
SUMMARIBS	AX194479	AX465429	AX194440 AX194481	AX194482	AX465390	AX465431	AE008951	_	LMFLCHR34 06	AC018659 _	BC008984	AY286020	AY172561 AY286019	AC104336	AC133710	AC136491	AC022557	AU513473	BX323850	AX194475 AX194483	AX465425	AX465433	HSA339016	HSA330295	HSA338993 AX438770	HSA338994	AR387935 AX101989	HSU39195	AK100056		18	0410	ALI.		19 bp D1 Patent WO0151500.	35			and Verthelvi,D	and its use to 79 19-JUL-2001;
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PAT 28-AUG-2001

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Klinman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 81 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Oligodeoxynuclectide and its use to induce an immune response
Patent: WO 0151500-A 82 19-JUL-2001;
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Sequence 82 from Patent WO0151500.
AXI94482
AXI94482.1 GI:15385138
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Sequence 81 from Patent W00151500.
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                     Best Local Similarity 94.4
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Oligodeoxynuclectide and its use to induce an immune response
Patent: WO 0151500-A 40 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Vaccine against RSV
Patent: Wo 0211761-A 97 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Sequence 40 from Patent WO0151500.
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Sequence 97 from Patent W00211761.
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Agrobacterium tumefaciens str. C58 (U. Washington)
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

1 (bases 1 to 10007)
S. Wood, D.W. Setubal, J.C., Kaul, R., Wonks, D., Chen, L., Wood, G.E.,
Chen, Y., Woo, L., Kitajima, J.P., Okura, V. K., Almeida Jr., N. F.,
Zhou, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G.,
Giller, W., Garaft, C., Quenthner, D., Kutyavin, T., Levy, R., Li, M.,
McClelland, E., Palmieri, A., Raymond, C., Rouse, G.,
Saenphimmachak, C., Wu, Z., Gordon, D., Bisen, J.A., Paulsen, I.,
Krespan, W., Perry, M., Gordon, D., Bisen, J.A., Biddle, P., Jung, M.,
Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C.,
Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
and Nester, E.W.
The genome of the natural genetic engineer Agrobacterium
tumefaciens CS8
L. Science 294 (5550), 2317-2323 (2001)
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Agrobacterium tumefaciens str. C58 AT plasmid section 26 of 49 of
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Vaccine against RSV
Patent: WO 0211761-A 100 14-PEB-2002;
HENRY M. ACKSON POUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Submitted (27-SEP-2001) Department of Microbiology, Un
Washington, 1959 NB Pacific Ave, Box 357242, Seattle, '
98195-7242, USA
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94.4%; Pred. No. 2.8e+03;
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Vaccine against RSV
Vaccine against RSV
Barent: WO 0211761-A 58 14-PEB-2002,
PERRY W JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Vaccine against RSV
Vaccine against RSV
Batch: WO 0211761-A 99 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Sequence 100 from Patent WO0211761.
AX465432
AX465432.1 GI:21899795
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Sequence 99 from Patent WO0211761.
AX465431
                                          20 bp
Sequence 58 from Patent WO0211761.
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TGCGTCGATGCAGGGGGG 20
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                                                                                                           AX465390.1 GI:21899753
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Best Local Similarity
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AUTHORS
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RESULT 6
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AX465432
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                                                                                                                                                                                                                                                                   complement(731..1860)
complement(731..1860)
fonce = "AtubSagu"
fonce = "AtubSagu"
fonce start = lastx/Glimmer"
fonce start = lastx/Glimmer
fonce start = lastx/Gli
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ALEVYRTITENRHYHLJVI BADRANASIWYPMARDGALIUDAANDDFHYLHYUTYNBEG
GIYBD PASR PYRHLARSLATGFVYGGEPR PSRNFAASGEPSGELLDPREVNDFHHYDRO
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BOST BINRLAGABS FGGELF PRASGWYNDPNDGHTWQLSTLKWTHAETYBGRQSRADMA
ALLARKRGHI WPLLGCFFFRGI SLOCEPRCLAID DWHFKAGRLEMRANLSENWCELPAV
KGEILHRNGSVQNITRYEGYAAQPAIYAGR
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ALERAISAYRDRELFRRLQTQAMQANFSWDKSAAQYMALFESLVGNSTRETDAVADIR
TETFAKIRADRRLAGTPGSTG**
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complement (1923. ,4336)
/gene="Atu5286"
/note="putative, ORF located using Glimmer"
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                                                                                                                                                                                       complement (73. .1860)
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E (bases 1 to 11009)

(S Hinkle,G., Slater,S.C. and Goodner,B.

S Hinkle,G., Slater,S.C. and Goodner,B.

Direct Submission

U Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,

Cambridge, MA 02139, UGA

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Agrobacterium tumefaciens str. C58 (Cereon)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
1 (bases 1 to 11009)
Hinkled G., Slater, S.C. and Goodner, B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
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8428. .8847
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                                                                                            Query Match 91.1%; Score 16.4; DB 1; Length 11009; Best Local Similarity 94.4%; Pred. No. 1.2e+03; Matches 17; Conservative 0; Mismatches 1; Indels 0;
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Fragment Name
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LMFLCHR32 15
LMFLCHR32 16
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LMFLCHR32
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LMFLCHR34_06
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7411. 8076

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of Sequence similarity are identified by BLAST (GNC. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                   Department
                                                                                                                                                                                                                                                                                                                   Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (31-MAY-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 178145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (18-MAR-2003) Human Genome Sequencing Center, Departmen Submitted (18-MAR-2003) Human Genome Sequencing Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14269664.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                            Submitted (16-DBC-1999) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                      Submitted (01-UDN-2001) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-JUN-2001) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

[Dases 1 to 178145]
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4 (bases 1 to 178145)
                                         (bases 1 to 178145)
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                                                               Worley, K.C.
Direct Submission
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Bukaryotz Hotolary, Primates; Catarrhini, Hominidae; Homo.

I (bases 1 to 1734).

Murny D. M. Adams. C., Adio-Oduola, B., Ali-osman, F. R., Alian, C., Alabrooks, Silevae, M., Brown, M., Banks, T., Barbaria, J., Benton, J., Edwazos, S. L., Adio-Oduola, B., Alian, C., Barbaria, J., Burch, P., Burkett, C., Burchill, K.L., Byrd, N.C., Carron, T.F., Carrot, T.F., Carrot, T.F., Carrot, C., Coyle, M.D., Dathorne, S. M. David, N.C., Carrot, T.F., Carrot, T.F., Carrot, J., Chang, D., Chave, D., Chen, R., Carrot, T.F., Carrot, J. Chen, S., Carrot, J. M., D., Dathorne, S. M. David, N.C., Carrot, T.F., Carrot, J. Chen, S., Dend, M. D., Dathorne, S. M. David, M. D., Dathorne, S. M. David, M. D., Dathorne, S. David, M. David, J. Edward, C. Coyle, M. D., Dathorne, S. M. David, M. David, J. Edward, C. Coyle, M. D., Dathorne, S. M., Douthwaite, M. J., Edward, J. Harla, M. Havlak, P. Hale, S., Hamilton, K., Han, J., Harla, M. Havlak, P. Hale, S., Hamilton, K., Harla, M. Harla, M. Havlak, P. Hale, S., Hamilton, K., Harla, M. Harla, M. Havlak, P. Hale, S., Hamilton, K., Harla, M. Harla, M. Havlak, P. Hale, S., Hamilton, K., Harla, M. Harla, M. Mathorne, M. Martindale, A., Martindale, A., Martindale, M., Mathorne, M. Martindale, A., Mathorne, M. Martindale, M., Mathorne, M. Martindale, M., Mathorne, M. Martindale, M., Mathorne, M. Martindale, A., Mathorne, M. Martindale, M., Mathorne, M. Martindale, M., Mathorne, M. Martindale, M., Mathorne, M. 
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Homo sapiens 12 BAC RPI1-528MI8 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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Pred. No. 9.2e+02;
0; Mismatches 1;
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Homo sapiens
      1100001
1200001
1300001
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Matches 17; Conservative
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Continuation (7 of 18) ob
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us-10-068-160-20.rge

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hypothetical protein from Mycobacterium tuberculosis (151 aa) fasta scores; opt: 639, z-score: 785.9, g(), (60.8% identity in 148 aa overlap) and SW: NODN RHILV nodulation protein from Rhizobium leguminosarum (161 aa) fasta scores; opt: 388, z-score: 482.2, E(): 1.6e-19, (44.8% identity in 145 aa overlap)"
                                                                                                                                                                                                                                                                                                                                    283100 bNA linear BCT 11-FEB-2003
Streptomyces coelicolor A3(2) complete genome; segment 7/29:
AL939110 AL035591 AL07932 AL096743 AL096811 AL096839 AL096844
AL096849 AL109848 AL132644 AL445403 AL513407 AL591322 AL645882
AL939110.1 GI:24413753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L., Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M., Cronin, A., Praser, A., Brown, S., Chandra, G., Chen, C.W., Collins, M., Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neil, S., Rabbinowitsch, E., Rajandraam, M.A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrell, B.G., Parkhill, J. and Hopwood, D.A.

Complete genome sequence of the model actinomycete Streptomyces Coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 283100)

2 (bases 1 to 283100)

Bentley,S.D.

Direct Submission

Submitted (19-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA B-mail: sdb@sanger.ac.uk

On or before Oct 26, 2002 this sequence version replaced

gi:20520819, gi:20520889, gi:20520880, gi:20520891, gi:20520704, gi:2052070
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                          Length 178145;
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/strain="A3(2)"
/db_xref="taxon:100226"
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                                                                                                              1; Indels
                                                    Score 16.4; DB 9;
Pred. No. 8.6e+02;
0; Mismatches 1;
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/note="synonym: SCI30A.19"
59. .520
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                                                       Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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KEYWORDS
SOURCE
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                                                                                                                                                                                                   note="overlaps bases 81513. .83601 of clone AC007424"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alusg"
complement(1816) . 18136)
/rpt_family="Alusg" . 21485)
/rpt_family="Light" . 21793)
/rpt_family="Rhuy"
complement(21486 . 21793)
/rpt_family="Liphg" . 24659)
/rpt_family="Liphg" . 25659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt family="Trich"
complement (11829 . 14890)
/rpt family="LIMBC"
complement (14986 . 15129)
/rpt family="MIR"
                                                                                                                                                                                                                                                                    /standard name="152792"
complement(5931. 6187)
/rpt family="MLT2CB"
complement(6208. 6289)
/rpt family="L2"
6933. 7081
/rpt family="CT-rich"
8001. 8036
/rpt family="AT_rich"
8243. 8568
/rpt family="AT_rich"
/rpt family="AT_rich"
/rpt family="AT_rich"
/rpt family="AT_rich"
/rpt family="AT_rich"
/rpt family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt family="Alusx" omplement(17811, .1812; rpt_family="Alusx")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="LIMB6"
complement(27004..27312)
/rpt_family="AluSx"
27304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt family="MiR"
complement(11452, :1536)
rpt family="LIMBC"
1538, :11772
                                                                                                                                                                                                                               function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="(TATG)n"
5802. .25961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="LIMB6"
28322. .28626
/rpt_family="L2"
28990. .29026
                                                          chromosome="12"
clone="RP11-528M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt family="A-rich" 0871. .11106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="MER103"
5757. .27003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="THE1B"
5438. .25507
                                                                                                              . .5920
rpt_family="L1PA5"
. .2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7313. .27340
rpt_family="L1MB6"
7341. .27636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="MIR"
1247. .11375
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gene

SGS

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2850. .3491
2850. .3491
2850. .3491
// Gene="SCO1702"
// note="SCO1702"
// note="SCO1702"
// note="SCO1702"
// note="SCO130A.23"
// note="SCO1702"
// note="SCO130A.23"
// note="
/db_xref="GOA:098251"
/db xref="GOA:098251"
/db xref="SPTREMBL:098251"
/translation="MNLELSEEGTAVRQLARDFVEREIAPHVVEWDRABEVDRSLVKK
LGEWGFLGITIDBGYGGSGGOHLAYCLIVTBELGGEGSSVRGITVSVSLGLVAKTJAAWG
DEEQKRANLPGLISGETVGCFGLITPDGTGSBAGNLTPRAVRDGDDYVVAKTYTAAWG
TWADVVLLPRASTDAFGHQVYSAFLVPTDTPGLITRRTHGKLGIRGQATAELVTBOV
VPASAMLAPEGKGFSVAMSALAKGRNSVAAGCVGIAQAALDAAVRYAGEREQFGKTIA
HHQLVQELISDIALDVDAARRLTWRYADLIDRGQPFAYESSKAMLFASERAVRAANNA
LQVFQAYGYIDEYPAGKLLRDARVWTLYEGTSQIQKLVIGRALFGVSAF"
/gone="SCO1701"
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2737a; similar to many eg. SW:NERR STRLI probable mercury
resistance operon repressor from Streptomyces lividans
(125 an fasta scores; opt: 144, z-score: 183.3, E():
0.007, (181.24 identity in 89 aa overlap). Contains Pfam
match to entry PF01022 HTH 5, Bacterial regulatory
protein, arsk family. Contains possible helix-turn-helix
/codom start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2925. .3017
/gene="SCO1702"
/note="PS01081 Bacterial regulatory proteins, tetR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF00441 Acyl-CoA dh, Acyl-CoA dehydrogenase, score 565.20, E-value 4.3e-166."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2889. .3029
/gene="SCO1702"
/note="Pfam match to entry PF00440 tetR, Bacterial
regulatory proteins, tetR family, score 45.00, B-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gabs
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/protein_id="C51848801.1"
/db_xref="G1:544177"
/db_xref="G2A:Q58249"
/db_xref="SPTREMBL:Q9S249"
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Pred. No. 8.1e+02;
0; Mismatches 1; Indele
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3555. .4268
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/gene="SCO1703"
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/gene="SCO1703"
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1 Similarity 94.48;
17; Conservative (
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCU104.20c, possible transcriptional regulator, /gene="SCU104.20c, possible transcriptional regulator, /note="SCU104.20c, possible transcriptional regulator, | len: 215 aa; similar to many e.g. TR:CAB39717 (EMB1:AL049485) putative regulatory protein from Streptcomyces coelicolor (221 aa) fasta scores; opt: 330, 2-score: 413.5, E(): 1.1e-15, (33.6% identity in 216 aa overlap) and R:AAD13556 (EMB1:AP060235) Lank regulator of landomycin biosynthesis in Streptcomyces cyanogenus 8136 (192 aa) fasta scores; opt: 170, z-score: 218.6, E(): 7.6e-05, (31.8% identity in 126 aa overlap). Contains Pfammatch to entry PP00440 terR, Bacterial regulatory proteins, terR family. Contains possible helix-turn-helix motif (44.32 SU) 43-64aa."

/codon start=1 /product="putative transcriptional regulator" /product="putative transcriptional regulator" /db_xref="GA3497971" /db_xref="GA3497971" /db_xref="GA34987971" /db_xref="GA3498781" /d
                                                                       /translation="MAEPRIFASADBVKAAVGEQLGYTDWLEVDQKRIDLFAEATGDH
QWIHVDPERAAAGPFGGTIAHGYLTLSLLPLFGPQLIRVDGVKWGVNYGTNKVRFPSP
VPVGSRLRATAVITGVEDVKGGIQVSVAFTVERBGGDKPVCVAESVSRYYL"
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fagnes "SCO1700"

/note="synonym: SCI30A.21c"

complement (1219. .1533)

fagnes "SCO1700"

/note="SCI30A.21c, putative membrane protein, len: 104 aa.

Contains possible hydrophobic membrane spanning regions"
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383 aa; similar to many both prokaryote and eukaryote eg.
884.ACDB BACSU acyl-CoA dehydrogenase from Bacillus
subrilis (379 aa) fasta scores; opt: 109,1 z-score:
1197.8, E(): 0, (43.8% identity in 377 aa overlap) and
SW:ACDS RAT acyl-CoA dehydrogenase from Rattus norvegicus
E(at) (44.6% identity in 372 aa overlap). Contains Pfam
match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 60.70, E-value
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/protein_id="CAB46799.1"
/db_xref="GI:5441775"
                                                                                                                                                                                                                                                                            /note="synonym: SC130A.20c"
complement(511, 1158)
/gene="SCO1699"
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complement(1609..2760)
                                   xref="SPTREMBL:098254"
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                                                                                                                                                                                                complement (511. .1158) /gene="SCO1699"
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gene

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Search completed: July 2, 2004, 10:08:13 Job time : 636.732 secs

153387 TGCGGCGTGCAGGGGG 153404

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USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contect: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
  1166 bp mRNA linear PRI 12-JUL-2001
INAGE:4338853, mRNA, complete cds. FLJ23476, clone MGC:16780
BC008984.1 GI:14290439
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Place: 12 Row: o Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10440178. Location/Qualifiers
                                                                                                                                                                                 MGC.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/clone="MGC:16780 INAGE:4338853"
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/lab_nost="DHI08"
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/organism="Homo sapiens"
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                                                                         DEFINITION
                                                                                                                                                                                                                                       ORGANISM
RESULT 15
BC008984
                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT
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Sequence 3 Sequence 3 Sequence 3 Sequence

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Length 107;
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Pred. No. 1e+02;
0; Mismatches 2;
US-08-468-700-33
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Fatent No. 6410295
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Stagatd-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Alba-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/09/537,168
CURRENT FILING DATE: 2000-03-29
EARLIER FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/127,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Situlff, S ren
APPLICANT: Biggard-Frantzen, Henrik
APPLICANT: Biggard-Frantzen, Henrik
ITTLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709-000-02
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT APPLICATION NUMBER: US/09/193,068
SOFTWARE: PESTSEQ for Windows Version 3.0
SOFTWARE: PESTSEQ for Windows Version 3.0
ENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 21, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
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CTHER INFORMATION: n = a, c, g,
US-09-193-068-21
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Best Local Similarity 88.9%;
Matches 16; Conservative

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     RESULT 2
US-09-537-168-1
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Sequence 1, Appli
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Sequence 12,
Sequence 12,
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Sequence 1, P
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(c) 1993 - 2004 Compugen Ltd.
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US-09-814-052-5
US-08-812-829-5
US-08-164-422-33
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US-08-68-389-1
US-08-68-389-1
US-08-68-388A-1
US-08-68-88A-1
US-09-170-670-12
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US-09-672-459-1
US-09-636-252A-1
US-09-545-586-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB
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Gaps

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969 TGCATCGACACAGGGAGG 986

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STREET: 405 Lex
CITY: New York
STATE: New York
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STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: NEW YORK
COURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,052
FILING DATE: G-MAR-1997
CLASSIFICATION: 510
ATTORNEY/AGRATION:
NAME: Lambiris, Rilas J
REGISTRANCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4684.204-US
TELECHMANICATION INFORMATION:
TELECHMANICATION INFORMATION:
TELECHMANICATION INFORMATION:
TELECHMANICATION INFORMATION:
TELERRANCE/DOCKET NUMBER: 32,728
TELERRANCE/DOCKET NUMBER: 32,728
TELERRANCE/DOCKET NUMBER: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                ö
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APPLICANT: von der Osten, Claus
APPLICANT: derry, Joel R.

APPLICANT: Bjornvad, Mads E.

APPLICANT: Bjornvad, Mads E.

APPLICANT: Wind, Jesper
APPLICANT: Wind, Jesper
APPLICANT: Wasaussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                       Query Match 82.2%; Score 14.8; DB 4; Length 1443; Best Local Similarity 88.9%; Pred: No. 1.1e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; Score 14.8; DB 3; Length 1683; 88.9%; Pred. No. 1.16+02; tive 0; Mismatches 2; Indels 0
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                 LENGTH: 1443
TYPE: DNA
ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08814052
Patent No. 6015783
                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 réchréchénédades 893
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Best Local Similarity 88.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                ; NAME/KBY: CDS
; LOCATION: (1)...(1443)
US-09-537-168-1
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STRANDEDNESS
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3: No. 60177510 No. 6017751disk of No. 6017751th America, Inc. 405 Lexington Avenue, Suite 6400
                     GENERAL INFORMATION:
APPLICANT: Von der Osten, Claus
APPLICANT: Von der Osten, Claus
APPLICANT: Vind, Jesper
APPLICANT: Vind, Jesper
APPLICANT: Rasmussen, Michael Dolberg
TITLB OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLB OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60177510 No. 6017751disk of No. 601775101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.2%; Score 14.9; DB 3;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FRACESQ FOr Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,829
FILING DATE: 06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VAN COLOEN, ALBERT J. J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: SEN, JAN
APPLICANT: SIJNONS, PETER C.
APPLICANT: QURX, WILHEMUS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/08146422
Patent No. 5543576
Sequence 5, Application US/08812829
Patent No. 6017751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,728
                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
WEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 06-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1683 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
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Sequence 16, Application US/08626554

Betent No. 5714474

GENERAL INFORMATION:
APPLICANT: WAN OOLIEN, ALBERT J.J.
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: BIN, JAN.
APPLICANT: SIDMONS, PETER C.
APPLICANT: VERNORED, TEUNIS C.
APPLICANT: WERNORED, TEUNIS C.
APPLICANT: WENDUCTION OF ENZYMES IN SEEDS AND THEIR TITLE OF INVENTION: USB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8; DB 1; Length 1777;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DC.
CONTRY: USA
ZIP: 2006-1888
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,554
FILING DATE: 02-APR-1996
TLASSIPICATION: 514
ATTORNEY FAGENT INFORMATION:
NAME: MUMBER: 26192-20011.10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICA
                                 ATTORNEY CATELY
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,919.
REPERENCE/DOCKET NUMBER: 24615-20033.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELERIOR (415) 813-5600
TELERIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 32
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 PENNSYLVANIA AVENUE NW
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 rechrechenchedeade 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.2%;
Best Local Similarity 88.9%;
Matches 16; Conservative (
         FILING DATE: 12-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-626-554-16
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US-08-626-554-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FACENT NO. 3'0.34'D.

GENERAL INCORMATION:
APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: CORA, WILHELMUS J.
APPLICANT: CORA, WILHELMUS J.
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
ITILE OF INVENTION: TRANSGENIC PLANTS HAVING A MODIFIED
TITLE OF INVENTION: CARBOHYDRATE CONTENT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & POERSTER
STREET: 755 PAGE Mill Road
CITY: Palo Alto
STREET: 755 PAGE MILL ROAD
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION NUMBER: US/08/253,575
APPLICANTON NUMBER: US/08/253,575
                                                                                                                                                                                                    CUDNIKK: 0.204

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I3M FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,422
FILING DATE: 02-NOV-1993
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 44615-20011.23
TELECOMMUNICATION: INFORMATION:
TELEFECOMMUNICATION: 1812-5600
TELEFEX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
RICK APPLICATION DATA:
RAPPLICATION NUMBER: US 07/849,422
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08253575
Patent No. 5705375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 TGCATCGACACAGGGAGG 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-146-422-33
                                                                                                                                                                                     USA
                                                                                               CITY: Pa.
STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-253-575-1
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us-10-068-160-19.rni

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TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 60177510 No. 6017751disk of No. 6017751th America, Inc.
STATE: 405 Lexington Avenue, Suite 6400
CITY: New York
COUNTRY: US.A.
ZIP: 10174-641;
COMPUTRY: US.A.
ZIP: 10174-641;
COMPUTRY: BW COMPAIDE DISKette
COMPUTRY: BW COMPAIDE DISKette
COMPUTRY: BW COMPAIDE
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Patent No. 6287826

GENERAL INFORMATION:
APPLICANT: No. 6287826man, Barrie Edmund
APPLICANT: No. 6287826man, Barrie Edmund
TITLE OF INVENTION: Ensymatic Preparation of Glucose Syrup
TITLE OF INVENTION: Prom Starch
TITLE OF INVENTION: Prom Starch
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1999-03-08
EARLIER FILING DATE: 1998-03-09
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 1

LENTH. 1912
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Pred. No. 1.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGCATCGACGCAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: mat peptide
; LOCATION: (421)...(186
US-09-264-097-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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MOLECULE TYPE:

US-08-812-829-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 60157830 No. 6015783disk of No. 6015783th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BM Compatible
OFFRATING SYSTEM: OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
CLASSIFICATION: 510
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                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: von der Osten, Claus
APPLICANT: horry, Joel R.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Samussen, Michael Dolberg
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
TITLE OF INVENTION: 55
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         82.2%; Score 14.8; DB 1; Length 1777; 88.9%; Pred. No. 1.1e+02; ive 0; Mismatches 2; Indels 0
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88.9%; Pred. No. 1.1e+02;
ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         von der Osten, Claus
Bjornvad, Mads E.
Vind, Jesper
Rasmussen, Michael Dolberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REPRENCE/DOCKET NUMBER: 4684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08812829
Patent No. 6017751
GENERAL INFORMATION:
APPLICANT: von der Osten, Claus
APPLICANT: Bjornvad, Mads E.
                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/08814052; Patent No. 6015783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1323 rechreachedededed 1340
                                                                                                                                                                                            978 TGCATCGACACAGGAGG 995
                                                                                                                                    1 TGCATCGACGCAGGGGG 18
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SEQUENCE CHARACTERISTICS:
LENGTH: 1893 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
      Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16, Conservative
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TELEX:
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Length 1893;

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SSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc. 1405 Lexington Avenue, 64th Floor
New York
New York
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Pred. No. 1.18+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: US-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY DATE: ASTONEY DATE: 
Sequence 1, Application US/08459610; Sequence 1, Application US/08459610; Patent No. 5801043; APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Brochert, Torben Vedel APPLICANT: Svendsen, Allan APPLICANT: Thelleren, Marianne APPLICANT: Van der Zee, Pia TILLE OF INVENTION: AMYLASE VARIANTS NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS: ADDRESSER: AOS TREET: 405 Learner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NESULT 13
US-08-343-804-1
Sequence 1, Application US/08343804
Setent No. 5830837
GENERAL INFORMATION:
APPLICANT: Biggard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY USA
ZIP: 10174-6401
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.9
Matches 16; Conservative
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421..1869
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STRANDEDNESS: single
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334..1872
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FEATURE:
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LOCATION:
FEATURE:
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LOCATION:
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; LOCATION:
US-08-459-610-1
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APPLICANT: Biggaard Frantzen, Henrik
APPLICANT: Bordhert, Torben Vedel
APPLICANT: Borchert, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pla
APPLICANT: Van der Zee, Pla
TILLE OF INVENTION: ANTIASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSE:
ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
CITY: New York
STATE: New York
COUNTRY: USA
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                                                               n 82.2%; Score 14.8; DB 3; Length 1918; Similarity 88.9%; Pred, No. 1.1e+02; 16. Conservative 0; Mismatches 2; Indels 0;
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82.2%; Score 14.8; DB 1; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/720,899

FILING DATE: 10-OCT-1996

CLASSIPICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: A35

PRIOR APPLICATION: A35

PRIOR APPLICATION: A35

TELING DATE: 22-NOV-1994

ATTORNBY/AGENT INPORMATION:

NAME: Lowney Dr., Karen A.

REFISHANCE/DOCKET NUMBER: 4054.214-US

TELEFARA: 212-867-0123

TELEFARA: 212-871-015
                                                                                                                                                                                                                                                       1302 recarceacacacacace 1319
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US-08-720-899-1
; Sequence 1, Application US/08720899
; Patent No. 5753460
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 334..1872
FEATURE:
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421..1869
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, LOCATION;
US-08-720-899-1
                                                               Query Match
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Gaps

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Sequence 1, Application US/08600908A
Sequence 1, Application US/08600908A
Barent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc. STREET: AS Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.2%; Score 14.8; DB 2; Length 1920; Best Local Similarity 88.9%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0.
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,399
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4127.204-US
TELEPHONE: 212-87-0123
TELEPHONE: 212-87-0123
TELEPHONE: CHARACTERISTICS:
SEQUENT: 1920 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COMPRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PREADING Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION *435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/POCKET NUMBER: 38,475
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; LOCATION: 421..1869
US-08-687-399-1
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                            APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
ATILES OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
NUMBER OF SEQUENCES: 38
ADDRESSER: No. 58308370 No. 5830837disk of No. 5830837th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
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STREET: 405 Lexington Avenue, 64th Floor
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88.9%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels 0
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US-08-687-399-1
; Sequence 1, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
APPLICANT: Toft, Annette H.
APPLICANT: Pederset, Hanne H.
APPLICANT: Nilsson, Thomas B.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
TITLE OF INVENTION: Process
NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                     STATE: New York COUNTRY: United States of America ZIP: 10174-6401 COMPUTER REALABLE FORM:
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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334..1872
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LOCATION:
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LOCATION:
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LOCATION:
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; TELEPAX: 212-878-9655
; INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1920 base pairs yer.
; FRANDEDNES: single TYPE: nucleic acid STRANDEDNES: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FRATURE: DOCATION: 334.1869
; RAFIURE: NAME/KEY: BIG PEPTIDE: NAME/KEY: BIG PEPTIDE: NAME/KEY: BIG PEPTIDE: NAME/KEY: MATURE/KEY: MATURE/
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Search completed: July 2, 2004, 13:37:53 Job time: 29.2073 secs

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2, 2004, 06:05:50 ; Search time 134.89 Seconds (without alignments) 566.887 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                    3373863 seqs, 2124099041 residues
                                                                using sw model
                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                    1 tgcatcgacgcagggggg 18
                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
                                                                                                                                                                  US-10-068-160-19
18
                                                                - nucleic search,
                                                                                                July
                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                              OM nucleic
                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                    Searched:
                                                                                                Run on:
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genesegn2001as:\* geneseqn2003as:\* genesegn2000s:\* geneseqn2002s:\* geneseqn2001bs

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:\* geneseqn2003bs:\* geneseqn2003cs:\* genesegn1980s:\* geneseqn2004s: 8: 9: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

uoj	Immunorea	Immunosti	Immunosti	Immunosti	CpG oligo	CpG oligo	D class C	CpG D oli	Immunosti	Immunosti	Immunogen	Immunorea	Immunosti	Immunosti	Immunosti	Immunosti	CpG D oli	Immunogen	Immunogen	Immunogen	Immunogen	Immunogen	Immunogen
Description	AaB09650	Ab135616	Ab135572	Ab135583	Acc48314	Acc48304	Acc83119	Add01057	Ab135605	Ab135593	Aac80668	Aas09638	Abk46516	Ab135587	Ab135577	Ab135625	Add01052	Aac80619	Aac80621	Aac80652	Aac80614	Aac80612	Aac80617
SUMMARIES	AAS09650	ABL35616	ABL35572	ABL35583	ACC48314	ACC48304	ACC83119	ADD01057	ABL35605	ABL35593	AAC80668	AAS09638	ABK46516	ABL35587	ABL35577	ABL35625	ADD01052	AAC80619	AAC80621	AAC80652	AAC80614	AAC80612	AAC80617
88	4	o.	ø	ω	۲-	7	ω	o	φ	φ	4	4	9	9	9	9	φ	4	T	4	4	4	4
Length DB	20	20	20	20	20	20	20	20	28	23	19	19	13	89 r1	¥8	19	8	20	20	20	20	20	20
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.4	94.4	94.4	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1
Score		18	18	18	18	18	18	18	18	18	17	17	17	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
Result No.	п	7	m	4	ιΩ	φ	7	60	σn	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Immunogen	Immunogen	Immunorea	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti	Immunosti							
Aac80618	Aac80623	Aas09622	Aas09591	Aas09582	Aas09587	Aas09589	Aas09593	AaB09584	Aas09588	Ab135576	Ab135586	Ab135568	Ab135624	Ab135579	Ab135620	Ab135612	Abk46500	Abk46469	Abk46460	Abk46465	Abk46471
AAC80618	AAC80623	AAS09622	AAS09591	AAS09582	AAS09587	AAS09589	AAS09593	AAS09584	AAS09588	ABL35576	ABL35586	ABL35568	ABL35624	ABL35579	ABL35620	ABL35612	ABK46500	ABK46469	ABK46460	ABK46465	ABK46471
4	4	4	4	4	4	4	4	4	<; ₩	<b>4</b>	<u>ح</u>	9	•	•	<b>ب</b> ة و	<u>ج</u> 9	« «	K	κ. 	<u>د</u>	α,
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~	2	N	N	~	7	C)	~	7	7	7	7	7	7	7	2	2	20	2	7	20	7
91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1
16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
24	25	26	27	28	50	30	31	32	e e e	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

CpG sequence; immune response; non-B cell activation; interferon gamma; therageutici allergy; asthma; carcer; autoimmune disorder; interleukin-6 production; therageutici allergy; asthma; cancer; autoimmune disorder; intection; blo-warfare; vaccine; autisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Rbola; Anthrax; Listeria; se. Immunoreactive CpG sequence-containing oligonucleotide #100. AAS09650 standard; DNA; 20 BP. (first entry) 26-SEP-2001 AAS09650; 

12-JAN-2001; 2001WO-US001122. WO200151500-A1. 19-JUL-2001. Synthetic.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES. ö Verthelyi Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences.

Claim 5; Page 43; 48pp; English.

AAS09551-AAS09662 represent oligodeoxynuclectides (ODN) of at least 10 nuclectides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The

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mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interlevin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allerapy. The ODN are useful for treating, preventing or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atoppic conditions, for improving the efficacy of vaccines cand other atoppic conditions. For improving the efficacy of vaccines cand other atoppic conditions. For improving the efficacy of vaccines cand other atoppic manue system deficiencies, e.g. lupus creating immune system deficiencies, e.g. lupus creating immune system deficiencies, e.g. lupus creating immune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Prancisella schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and contractions resulting from exposure of bio-warfare agent, including Bbola,
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/note= "optionally thymidine is replaced by uracil to

form RNA or DNA/RNA hybrids. Thymidine is linked to at

least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; allergy; cancer, hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
are useful for inducing an immune response, preferably a cell-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 4; Length 20;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulatory oligonucleotide SEQ ID NO: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGCATCGACGCAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL35616 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Anthrax and Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-130570/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200193902-A2
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misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mond JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL35616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL35616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .20 /*reag= a //oreagle //oreagle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunostimulatory compositions comprising RNA/DNA hybrid oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
cancer, allergy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 6; Length 20;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
particularly for treating diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
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                                                                                                                                            English.
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                                                                                                                                       Example 11; Page 62; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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cytokines, par
HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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x_8x_99999999999988
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Example 11; Page 61; 68pp; English.
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comprises at least one oligonuclectide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomes and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunosimulatory oligonucleotide described in the exemplification of composition, The present invention relates to an immunostimulatory the invention

Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

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100.0%; Score 18; DB 6; Length 20; 100.0%; Pred. No. 11; 0; Indels ive 0; Mismatches 0; Indels
              ilarity 100.0%;
Conservative C
              Local Similarity
les 18; Conserv
 Query Match
                               Matches
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1 TGCATCGACGCAGGGGG 18 3 recarceacecades 20 ò d

ABL35583 standard; DNA; 20 BP ABL35583; RESULT 4

(first entry) 04-APR-2002 Immunostimulatory oligonucleotide SEQ ID NO: 509.

DNA/RNA hybrid, phosphorothicate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

Synthetic

Location/Qualifiers misc RNA

1. .20 /\*tag= a /note="optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

WO200193902-A2

13-DEC-2001

07-JUN-2001; 2001WO-US018276.

07-JUN-2000; 2000US-0209797P.

(BIOS-) BIOSYNEXUS INC.

Klinman DM; WPI; 2002-130570/17. Flora M,

Mond JJ,

New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

Example 11; Page 61; 68pp; English.

comprises at least one oligonous at immunosimizatory comprises at least one oligonous comprises at least one oligonous of a management of the composition is useful for chancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme diseases, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of present invention relates to an immunostimulatory composition, which the invention \*

Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 18; DB 6; Length 20; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels 18; Conservative Similarity Query Match Best Local S Matches

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RESULT 5

뮴. ACC48314 standard; DNA; 20 ACC48314

ACC48314;

(first entry) 11-AUG-2003

CpG oligodeoxynucleotide DV30.

CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.

Synthetic.

WO2003020884-A2.

13-MAR-2003

13-AUG-2002; 2002WO-US025732.

14-AUG-2001; 2001US-0312190P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Klinman DM, Gursel M,

WPI; 2003-300874/29.

Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxymucleotide. 

Disclosure, Fig 8; 69pp; English.

The present sequence is that of CpG oligodeoxynucleotide DV30 of the invention. A claimed method for generating dendritic cells involves contacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxynucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature presentation. Mature dendritic cells are useful for tumonocherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes

TGCATCGACGCAGGGGGG 18 3 TGCATCGACGCAGGGG 20

BP.

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ACC83119 standard; DNA; 20
                                                                                         ACC83119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a D type CpG oligodeoxynucleotide that is an example of claimed D type oligodeoxynucleotides (see ACC48294) of the invention. Mature dendritic cells are obtained by contacting a dendritic cell precursor, such as a monocyte, with such an oligodeoxynucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                CpG oligodeoxynucleotide, dendritic cell; tumour; immunotherapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.
                                       Gaps
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                                                                                                                                                                                             CpG oligodeoxynucleotide used for dendritic cell maturation
                 100.0%; Score 18; DB 7; Length 20; 100.0%; Pred. No. 11;
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/note= "N is any base (especially G)
                                                                                                                                                                                                                                                                                                                                any base (especially G)
Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                          immunostimulant; gene therapy; ss
                                       Mismatches
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                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                           1 TGCATCGACGCAGGGGG 18
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                            100.0%;
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                                                                        3 TGCATCGACGCAGGGGG
                                      18; Conservative
                                                                                                                                                                                                                                                                                                                      /*tag=
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gursel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-300874/29.
                            Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
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misc difference
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                                                                                                                                                                                                                            cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klinman DM,
                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                      ACC48304;
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                                      Matches
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                                                                                                                       ACC48304
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The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilising agent and encapsulating a K type oligodeoxynucleotide (ODM) including a CpG motif. The invention is useful in pharmaceutical composition for impairing crowth of a solid tumour cell (e.g. human tumour cell) bearing an innerleukin-13 receptor in a subject; for stimulating an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly innucherapeutic response against tumours or stimulating an in vivo or con infectious agent e.g. virus, bacteria and furnagus. It is also useful for delivering oligodeoxynucleotides including a cype motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer cot), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever, bronchial or allergic asthma, utticaria, food allergies), autoimmune diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and multiple sclerosis) and psoriasis. The present sequence is a D class CpC oDN potentially useful for encapsulating in SSCL.
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                                                                                                                                                                       Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxymucleotide; tuberculosis; gytókine; leishmaniasais, AlDS-associated Kaposi's tumour; thyroid; cancer; allergy; eczeme; allergic rhinitis; coryza; hay fever; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; estima; utticaria; autoimmune disease; diabetes; rheumatoid arrbritis; CyG motif; interleutin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                      D class CpG ODN sequence useful for encapsulating in SSCL, DV30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joshi BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klinman DM, Gursel I, Ishii KJ, Kawakami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2002; 2002WO-US024235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001; 2001US-0308283P.
25-JUL-2002; 2002US-00206407.
(first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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27-AUG-2003
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Conservative

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TGCATCGACGCAGGGGG

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The present invention describes a method for inducing the production of vascular endothelial growth factor (VEGF) by a cell comprising contacting the cell with a CpG oligonucleotide and therefore inducing the production of VEGF by the cell. Also described: (1) inducing neovascularisation in a tissue, comprising introducing a CpG oligonucleotide into an area of the inducing neovascularisation in the area of the tissue; (2) promoting angiogenesis in an area of the subject where angiogenesis is desired, and so inducing neovascularisation in the area of the tissue; (2) promoting angiogenesis in an area of the subject where angiogenesis is desired, comprising information of angiogenesis in the subject where angiogenesis is desired, comprising information a CpG oligonucleotide to a non-human mammal and administering a CpG oligonucleotide to a non-human mammal and administering the agent to the mammal, where inhibition of angiogenesis in the enimal indicates that the capent is effective in inhibiting neovascularisation. The CpG oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic activities, and can be used in gene therapy. The method and the CpG oligonucleotides can be used in gene therapy. The method and the CpG oligonucleotides can be used in indicing angiogenesis or neovascularisation, such as in subjects with a skin graft, subjects who exhibit male pattern baldness, or subjects with a skin graft, subjects who contacterosis or ischaemia. The method may also be used in screening for represents a CpG oligonucleotide which is used in the exemplification of the rearent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing the production of vascular endothelial growth factor by a cell, useful for inducing angiogenesis, comprises contacting the cell with a CPG oligodeoxymucleotide.
                                                                                                                                                                                                                                                                                                                                 vascular endothelial growth factor; VEGF; CpG oligonucleotide; neovascularisation; angiogenesis; vulnerary; vasotropic; antiarteriosclerotic; gene therapy; skin graft; male pattern baldness; atherosclerosis; ischaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; SEQ ID NO 21; 37pp; English.
                                                                                                                                                                                                                                                                                         CpG D oligonuclectide SEQ ID NO:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rouse BT;
                          TGCATCGACGCAGGGGGG 20
1 TGCATCGACGCAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2002; 2002WO-US040955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001US-0343457P.
                                                                                                                                                      ADD01057 standard; DNA; 20
                                                                                                                                                                                                                                         01-JAN-2004 (first entry)
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas as arcomas), autoimmune diseases or allergies (e.g. allergic thinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                          1..28 "A*tag= a
/*tag= "optionally thymidine is replaced by uracil to
/note= "optionally thymidine is linked to at
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunostimulatory compositions comprising RNA/DNA hybrid oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                      infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimalent; antiallergic; cytostatic; antiancrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                      DNA/RNA hybrid; phosphorothicate backbone; immunostimulatory; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                     Immunostimulatory oligonucleotide SEQ ID NO: 531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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           20
                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US018276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2000; 2000US-0209797P.
3 TGCATCGACGCAGGGGG
                                                                                                        ABL35605 standard; DNA; 28
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOS-) BIOSYNEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130570/17
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                                                                                                                                                                                 04-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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misc_RNA
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                                                                                      ABL35605
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1 TGCATCGACGCAGGGGGG 18

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Gaps

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Query Match
100.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels

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Immunostimulatory oligonucleotide SEQ ID NO: 519
11 TGCATCGACGCAGGGGG 28
                                                                                                                     ABL35593 standard; DNA; 28
                                                                                                                                                                                                                     04-APR-2002 (first entry)
                                                                                                                                                                      ABL35593;
                                                                      RESULT 10
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infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss. DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

Synthetic.

1. .28
/\*teg= a
/notionally thymidine is replaced by uracil to
/note= "optionally thypids. Thymidine is linked to at
least one other base through a ribose sugar" Location/Qualifiers misc\_RNA

WO200193902-A2

13-DEC-2001

07-JUN-2001; 2001WO-US018276.

07-JUN-2000; 2000US-0209797P.

(BIOS-) BIOSYNEXUS INC.

Flora M,

Klinman DM;

WPI; 2002-130570/17.

Mond JJ,

New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

Example 11; Page 61; 68pp; English.

The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergic thinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 28 BP; 11 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 18; DB 6; Length 28; 100.0%; Pred. No. 11; 0; Indels Mismatches ö Conservative Local Similarity es 18; Conserv Query Match Matches

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1 TGCATCGACGCAGGGGG 18 Tecalcatecadedee 20

g à

RESULT 11 AAC80668

AAC80668 standard; DNA; 19 BP

AAC80668;

(first entry) 14-FEB-2001 Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:88.

cpg oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy, asthma; infection; bodcerial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple solerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss.

Synthetic.

WO200061151-A2

19-OCT-2000,

12-APR-2000; 2000WO-US009839.

99US-0128898P. 12-APR-1999;

(KLIN/) KLINMAN D.

(VERT/) VERTHELYI D. (ISHI/)

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 37; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides CG (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5-NNNT-CpG-WNNN-3' or 5-RY-CpG-RY -3'. The central CpG motif is unmerthylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant code degradation. The invention also relates to an oligonucleotide designant, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-composition comprising the oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-RNTW-CpG-RNN-3' cell-mediated response, and those of the sequence 5'-RN-CpG-RY-3' being able to induce a humoral response of the sequence 5'-RN-CpG-RY-3' being able to induce a demoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells cell-mediated or cell-mediated or natural killer (RN) cells. A cell-mediated or chumoral response can then occur by activation of T- or B-cells. The chumoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic conditions which may be treated include strail, fungal and protozoal infections such as tuberculosis, Ald in the treatment of an autoimmune elsone induction may also be used in the treatment of an autoimmune elsone elsone elsone induction in the treatment of an autoimmune elsone elson

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erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonuclectide, either alone or in combination with an anti-cancer oligonuclectide, either alone or in combination with an anti-cancer immunosers. The induction of an immune response is used in antisenes therapy and to improve the efficacy of a vaccine. The oligonuclectide is preferably administered to the present settivated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynuclectide of the invention
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Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

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Score 17; DB 4; Length 19;
Pred. No. 37;
                               0; Indels
                               Mismatches
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100.0%; Pre
0;
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RESULT 12

AAS09638;

AAS09638 standard; DNA; 19 BP

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #88.

CpG sequence; immune response; non-B cell activation; interferon gamma; thergamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

W0200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

ä Verthelyi Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences

Claim 5; Page 41; 48pp; English.

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from annother of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IRN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, 

system e.g. autoimmune disorder or an immune system deficiency, infection of a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the elificacy of a vaccine and used in antisense therapy. The ODN are useful for treating, preventing or manellorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines and other atopic conditions, for improving the efficacy of vaccines against hepatitis A. B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple solerosis, infections including Franciscalla, solistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AlbS), leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, e.g. solid tumour cancer, a disease associated with the immune Anthrax and Listeria

Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

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ABK46516 standard; DNA; 19 RESULT 13 ABK46516 

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(first entry) 05-JUN-2002 ABK46516;

unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine; Immunostimulatory unmethylated CpG oligodideoxynucleotide #106.

Paramyxoviridae, F protein, respiratory syncytial virus, RSV, viral bronchiolitis, pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.

Synthetic.

WO200211761-A2

14-FEB-2002.

09-AUG-2001; 2001WO-US041633

10-AUG-2000; 2000US-0224011P. 01-SBP-2000; 2000US-0229307P.

Klinman DM; Mond JJ, Prince G,

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

WPI; 2002-227118/28.

Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae P protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.

Claim 4; Page 9; 30pp; English.

φ The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond) oligodideoxynucleotides (ODNs). The vaccine is useful for vaccinating a patient especially against viruses the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have

Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA/RNA hybrid; phosphorothicate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bic-warfare; immunostimulant; antiallergic; cycostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprisant both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)nalignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhintis, hy fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfarre agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
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Query Match 91.1%; Score 16.4; DB 6; Length 18; Best Local Similarity 94.4%; Pred. No. 76; Matches 17; Conservative 0; Mismatches 1; Indels
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			2011/10/10/20	
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	score	Macch	rengtu	3	1D	Description
7	17	94.4	19	9	AX194476	476 Segn
N	17	٠.	19	9	AX465426	65426 Segment
			20	4	AX194440	4440 Segment
4			20	v	AX1944B1	AX194481 Semience
2	16.4		20	φ	AX194482	AX194482 Semence
9	Ġ.		20	φ	AX194501	AX194501 Segmence
7	16.4		20	φ	AX352203	AX352203 Sequence
80	Ġ.		20	φ	AX352214	AX352214 Seguence
σ	ė		20	9	AX352247	AX352247 Sequence
10	è.		20	ø	AX465390	AX465390 Sequence
11	Ġ		20	ø	AX465431	AX465431 Seguence
12	9		20	Ø	AX465432	AX465432 Sequence
13	9		28	ø	AX352224	AX352224 Sequence
14	ø		28	9	AX352236	AX352236 Sequence
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VERSION	X	AX194476.1	GI:15	53851	132	
KEYWORDS	٠					
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ORGANISM		ficial	sequence	วเร		
REFERENCE	H					

AX194476	
rocas	AX194476 19 bp DNA linear PAT 28-AUG-2001
DEFINITION	Sequence 76 from Patent WO0151500.
ACCESSION	AX194476
VERSION	AX194476.1 GI:15385132
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.
REFERENCE	H
AUTHORS	Klinman, D., Ishii, K. and Verthelyi, D.
TITLE	Oligodeoxynucleotide and its use to induce an immune response
JOURNAL	Patent: WO 0151500-A 76 19-JUL-2001;
	Secretary of the Department of Health and Human Services (HS)

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

SS Sonno, H. Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, S., Akahira, J., Hayatsu, M., Hirozane, T., Hori, F., Itahikawa, T., Itah, M., Izawa, M., Kadota, K., Kagawa, I., Ishikawa, T., Itah, M., Izawa, M., Kadota, K., Kagawa, I., Rai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shibata, Y., Shibata, K., Shibata, Y., Shibata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tamnoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, T. RIKEN Mouse ESTS (Konno, H., et al. 1999)

Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: B1-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Awai, J., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 465-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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(DH10B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Saskii,N.; Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.rtc.riken.go.jp)
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                                                                                                                             Fax: 81-45-503-9226

Fax: 81-45-503-9226

Email: genome-reseges.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Sasaki,N., Izawa,M., Watahiki,M., Okazaki,Y. and
Hayashizaki,Y.
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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itch,M., Kitsunai,T., Shibata,K., Izawa,M., Kawai,J.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 [5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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             Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, adult male testis (DH108)"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Location/Qualifiers
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PEATURES

Query Match

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AQ831712
HS_2087_Al_C07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2087 Col=13 Row=E, genomic survey
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401 Queen Anne Avenue North, Seattle, WA 99109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Seq primer: T7
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 401)
Mahairas; G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
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E-Coli DH10B"
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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (basea 1 to 303)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Endo, T.,
Kai, C., Tshikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Nammra, M., Oda, H., Okazaki, Y.,
Matsuyama, T., Miki, R., Mitchi, N., Nammra, M., Oda, H., Okazaki, Y.,
Shibata, Y., Shigemoto, Y., Shiraki, T., Sagobe, Y., Shibata, K.,
Shibata, Y., Watahiki, A., Watanabhi, F., Tateno, M., Tominaga, N.,
Yokota, T., Yoshino, H., et al. 1999)
Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-reseges riken.go.jp,
URL:http://genome.gec.riken.go.jp,
Sasaki,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., wuramatsu,M., Okazaki,Y. and
Haysshizaki,Y. and
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                           AV269637

AV269637 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930544609 3', mRNA sequence.
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strain="c57BL/61"
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/clone="4930544G09"
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/dev_stage="adult"
/lab_host="DH108"
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Mus musculus
                           1 TGCATCGACGCAGGGG 18
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Best Local Similarity 94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadacaee: Chlamydomonas.

I (bases 1 to 693)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicallular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
Unwaniar Silvo Contact: Charles Hauser
Contact: Charles Hauser
Durbam, NC 27708-1000
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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1024037H01.yl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii CDNA, mRNA sequence.
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91.1%; Score 16.4; DB 12;
Best Local Similarity 94.4%; Pred. No. 5.1e+03;
Matches 17; Conservative 0; Mismatches 1;
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TGCATCGACTCAGGGGGG
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Tel: 919 613 8159
Fax: 919 613 8177
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CG458105 888 bp DNA linear GSS 17-SEP-2003 PUFXO21TDC ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0756C17, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, PACCAD
clade; Panicoideae; Andropogoneae; Zea.
clade; Panicoideae; Andropogoneae; Zea.

1 {bases 1 to 878}

Whitelawo.C.A., Quackenbush.J., Van Aken,S., Utterback,T.,
Rendick,A., Fraser.C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Outberlinshed (2002)
Other_GSSs: OGZAN65TV
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/clone="ZAWBMa074KIO"
/clone lib="ZM-0.7 l.5_KB"
/note="Vector: pBCSK-; Site 1: Hincil; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
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9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-5208
Email: Whitelaw@tigr.org
Seq primer: TR
Class: Sheared, ends.
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Pred. No. 5.4e+03;
0; Mismatches 1; Indels
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/strain="B73"
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/mol type="genomic DNA"
/strain="B73"
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Unpublished (2003)
Other GSSs: PUFXO21TBC
Contact: Cathy Whitelaw
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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1. .980
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: FF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 TCCATCGACGCAGGGGG 285
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                                                                                                                                                                                                                                                                         CG225423 960 bp DNA linear GSS 22-AUG-2003 OG2ANG5TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0744Kl0, genomic survey sequence. CG222423 CG225423.1 GI:34125311
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1 (Daaes 1 to 960)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Onnoblished (2002)
Other GSSs: OGZANGSTH
Contact: Cathy Whitelaw
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pcR4-FOPO, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="Leaxon:4577"
/clone="ZMVBMa0744K10"
/clone="ZMVCTO"
/note="Workor: PBGSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
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18-13 301-838-5643
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                        1; Indels
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                                                                                  91.1%; Score 16.4; DB 29;
94.4%; Pred. No. 5.4e+03;
live 0; Mismatches 1;
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Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1;
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Class: sheared ends.
Location/Qualifiers
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CC655225.1 GI:32058344
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CG225423/c
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CC655225
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 246)
1 (b
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Exax: 81-45-503-9216
Email: genome-resegesc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 980)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, R.M., Praesr.C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Cltek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGULO70TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/clone="zMMBWa0469K19"
/clone lib="zM 0.7 1.5_KB"
/note="Woctor: pBcSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
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N91570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone lib="RIKEN full-length enriched, adult male testis
(PR10B)"
                                                          for DNA sequencing using RNA
5.A. 95 (7), 3455-3460 (1998)
Lbata, K., Izawa, M., Kawai, J.,
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1 (Dases 1 to 355)
1 (Bases 1 to 355)
1 (Bases 1 to 355)
1 (Bame, M. J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldow, M. F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
Lzawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
.. Carninci,P., Muramatsu,M., Okazaki,Y. and
               Marsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RN polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J. Ohanatu,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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85.6%; Score 15.4; DB 9; Length 246;
Best Local Similarity 94.1%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4921504P03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="testis"
'dev_stage="adult"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .246
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Glossina morsitans morsitans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="male"
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note="country: Zimbabwe; EST from adult gut infected with
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NA clone,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse8le10_q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
                                                                                        Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
Pathogen Sequencing Unit
Pathogen Sequencing Unit
Hinxton, Cambridge, Call 15A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
Hall clones with suffix qlc are reverse primer reads starting at 5 end of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Nerck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the This clone is available soyalty-free through LLNL; contact the Seq primer: ETPFinm: (info@image.llnl.gov) for further information. Seq primer: ETPFinm:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A35 bp mRNA linear BST 03-APR zb24g04.sl Soares fetal lung NbHL19W Home sapiens cDNA clone IMAGE:303030 3' similar to gb:J04760 TROPONIN I, SLOW SKELETAL MUSCLE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 435)
Hillier,L., Clark,N., Dubuque,T., Blliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Pargons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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    .355
/organism="Glossina morsitans"

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Pred. No. 1.2e+04;
0; Mismatches 1.
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response genes
Genome Biol, 4 (10), R63 (2003)
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ilarity 94.1%;
Conservative
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N91570.1 GI:1444897
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us-10-068-160-19.rst

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KEYWORDS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Zea mays
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BqlII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG714924 1119 - RescueMu Grid AA Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fal: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1119039 row: 42
Class: transposon-tagged.
1. 468
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xxcf="txxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                Length 435;
                                                                                                                                                                                                                                                                                               85.6%; Score 15.4; DB 14; Length 94.1%; Pred. No. 1.3e+04; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
/db_xref="taxon:9606"
/clone="IMAGE:303030"
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Best Local Similarity
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Email: generobidife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
RRPEAT IN THE SEQUENCE
Simple repeat STRAND (+) BLEMENT (A)n LOCATION [449,468].
PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIS07147 473 bp mRNA linear EST 08-APR-2002 BBI70025B20H07.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis mellifera cDNA clone BBI70025B20H07 5', mRNA sequence.
                                                                             DNA
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/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
Site_2: Not1; This BB17 cDNA library was generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apidae, Apis.

1 (Dases I to 473)

Whitfield C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, J.,

Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.B.

Annoteated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the homey bee

Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Būkaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. I was extracted from leaf strips, double digested using BamHI and BgllI, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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/strain="mixed strains of Buropean bees, predominantly
A.m. liqustica"
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                             ch 85.6%; Score 15.4; DB 29; Length 468; I Similarity 94.1%; Pred. No. 1.3e+04; 16; Conservative 0; Mismatches 1; Indels 0
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/dev stage="adult worker honey bee"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tatl: 217 265 0309
Fax: 217 244 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: TAATACCACTACACTATAGGG
BACKWARD: ATTAACCCTACTAAAG
BACKWARD: B170055B20 row: H column: C
Seq primer: AGCGGATAACAATTTCACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Apis mellifera"
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High quality sequence stop: 473.
Location/Qualifiers
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/clone="BB170025B20H07"
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Apis mellifera
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                                                                                                                                                                                                                                                                                                    Query Match
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I (bases i to 504)

11 (bases i to 504)

12 (bases i to 504)

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subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennor, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1812904 S04 bp mRNA linear BST 08-JUL-1999
22C9 Pine Lambda Zap Xylem library Pinus taeda cDNA, mRNA sequence.
A1812804
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Matches 16, Conservative
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170 recerciakeedeed 186 11 1 TGCATCGACGCGGGG ઠે 임 Search completed: July 2, 2004, 13:33:11 Job time : 1351.14 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:	<pre>July 2, 2004, 07:36:05; Search time 633.732 Seconds     (without alignments)     1231.080 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-10-068-160-19 18 1 tgcatcgacgcagggggg 18
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database .	GenEmbl:*  1: qb ba:*  2: qb hq:*  4: qb ba:*  5: qb ov:*  6: qb par:*  10: qb par:*  10: qb par:*  11: qb par:*  11: qb par:*  11: qb par:*  11: qb par:*  12: qb vi:*  13: qb vi:*  14: qb vi:*  15: em par:*  20: em par:*  21: em par:*  22: em par:*  23: em par:*  24: em pb:*  25: em par:*  26: em par:*  27: em par:*  28: em par:*  29: em vi:*  21: em par:*  21: em par:*  22: em par:*  23: em htg other:*  34: em htg other:*  35: em htg rod:*  36: em htg rod:*  37: em htg rod:*  38: em htg vii:*  39: em htg rod:*  39: em htg rod:*  30: em htg rod:*  31: em htg vii:*  31: em htg rod:*  32: em htg rod:*  33: em htg vii:*  34: em htg rod:*  35: em htg rod:*  36: em htg mar:*  37: em htg vii:*  38: em htg vii:*  39: em htg vii:*  39: em htg vii:*  30: em htg rod:*  30: em htg vii:*  30: em htg vii:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	AX194500 Sequence	AX352202 Sequence	AX352213 Sequence	AX352246 Sequence	AX352223 Sequence	AX352235 Sequence	appeared 85257XC	AX352207 Sequence	AX352217 Sequence	AX352255 Sequence	AX194432 Sequence	AX194434 Sequence	AX194437 Sequence	AXI94438 Sequence	AX19441 Segrence	AX194443 Sequence	AX194472 Sequence	AX352198 Sequence	AX352209 Sequence	AX352216 Sequence	AX352242 Sequence	AX352254 Sequence	AX465382 Sequence	AX465384 Sequence	AA46538/ Sequence AX465388 Sequence	AX465389 Sequence	AX465391 Sequence	AX465393 Sequence	AX816067 Segmence	AX352204 Sequence	AX352248 Sequence	AX352228 Sequence	າຕົ	Se.	Sequenc	AX352239 Sequence	Sequenc	-		DNA linear DAT 28-AHG-2001						induce an immune response
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100.0%; Score 18, DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 542 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Patent: WO 0193902-A 519 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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|db_xref="raxon:32630"
|noTe="Synthetic HDR"
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Sequence 542 from Patent WO0193902.
AX352246.1 GI:18617529
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 498.13-DEC-2001;
Biosynexus Incorporated (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 509 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
             1. .20
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Sequence 498 from Patent WO0193902.
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100.0%; Score 18; DB

Query Match

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Mond,J.J., Prince,G. and Klinman,D.M.
Vacchine against RSV
Patent: WO 0211761-A 106 14-PEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (UG)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 513 13.DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 503 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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91.1%; Score 16.4; DB 6;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1;
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100.0%; Pred. No. 9.6e+02;
vative 0; Mismatches 0;
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/db_xref="teaxon:32630"
/noTe="Synthetic HDR"
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/organism="synthetic construct"
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Sequence 513 from Patent WO0193902.
AX352217
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Sequence 503 from Patent W00193902.
AX352207
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AX352217
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                  PAT 06-FEB-2002
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Oligodeoxynuclectide and its use to induce an immune response
Patent: WO 0151500-A 88 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 531 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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100.0%; Pred. No. 9.6e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.9e+02;
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           AX352235 28 bp
Seguence 531 from Patent W00193902.
AX352235
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Sequence 88 from Patent W00151500.
AX194488
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                                                                AX352235.1 GI:18617518
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Best Local Similarity 100.0
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 37 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 34 19-JUL-2001,
Secretary Of the Department of Health and Human Services (US)
Location/Qualifiers
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Pred. No. 1.9e+03;
0; Mismatches 1;
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91.1%; Score 16.4; DB 6;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
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Sequence 34 from Patent WO0151500.
AXI94434.1 GI:15385090
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Sequence 37 from Patent WO0151500.
AX194437
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Sequence 38 from Patent WO0151500.
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91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 551 13-DEC-2001;
Biosynexus Incorporated (US)
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Pred. No. 1.9e+03;
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Sequence 551 from Patent W00193902.
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AX352255.1 GI:18617538
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Sequence 32 from Patent W00151500.
AX194432. GI:15385088
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ORGANISM synthetic construct

AUTHORS Klimman, D. 18hii, K. and Verthelyi, D.
TITLE Oligodeoxyruncleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 38 19-JUL-2001;

FRATURES
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JORGANISM Secretary of the Department of Health and Human Services (US)
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Search completed: July 2, 2004, 10:08:10 Job time : 633.732 secs

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 240)

S. Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Skonno, H., Itoh, M., Izawa, M., Kadeta, K., Kagawa, I., Ishikawa, T., Itoh, M., Izawa, M., Kadeta, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Kogawa, I., Matsuyama, T., Mixi, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Santo, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sughara, Y., Shibata, Y., Watahiki, H., Takahashi, F., Tateno, M., Tominaga, N., Tokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshiki, M. Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshiki, M. Watanabe, S., Yamamura, T., Yasunishi, A., Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
BC855889 1024037H0
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CC455825 CGULC/7TV
CC65525 CGULC/7TV
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CC723957 11119069G
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                                     CG225423
AV253722
BX566321
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CG714924
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AI812904
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EST.
Mus musculus (house mouse)
Mus musculus
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                           - nucleic search, using sw model
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Klinman, D., Ishii, K. and Verthelyi, D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A Bl 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Oligodeoxymuclectide and its use to induce an immune response
Patent: WO 0151500-A 82 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
Query Match 91.1%; Score 16.4; DB 6; Length 20; Best Local Similarity 94.4%; Pred. No. 2.2e+03; Matches 17; Conservative 0; Mismatches 1; Indels
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Sequence 81 from Patent WO0151500.
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Vaccine against RSV
Vaccine against RSV
Barent: W0 0211761-A 94 14-FEB-2002;
HENRY W. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Sequence 40 from Patent WO0151500.
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Sequence 94 from Patent WO0211761
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 iocation/Qualifiers
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                               Mond,J.J., Flora,M. and Klinman,D.M.
Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 510 13-DEC-2001;
Blosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 543 13-DEC-2001;
Biosynexus Incorporated (US)
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94.4%; Pred. No. 2.2e+03;
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Sequence 543 from Patent WO0193902.
AX352247
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Sequence 58 from Patent WO0211761.
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Oligodeoxynuclectide and its use to induce an immune response
Patent: WO 0151500-A 101 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 499 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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/db_xref="texon:32630"
/note="Synthetic HDR"
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Sequence 510 from Patent WO0193902.
AX352214
AX352214.1 GI:18617497
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Sequence 499 from Patent W00193902.
AX352203
AX352203.1 GI:18617486
                              AX194501 20 bp
Sequence 101 from Patent WO0151500.
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Vaccine against RSV
Vaccine against RSV
Batchir. WO 0211761-A 100 14-PEB-2002;
PERRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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                                                                                           Length 20;
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Mol type="unassigned DNA"
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"And 1 type="unassigned DNA"
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forganism="synthetic construct"
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fore="Synthetic oligonucleotide"
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Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1;
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Sequence 100 from Patent WO0211761.
AX465432
AX465432.1 GI:21899795
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AX465431
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 520 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Patent: WO 0193902-A 532 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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llarity 94.4%; Pred. No. 2.1e+03;
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Seguence 520 from Patent W00193902.
AX352224
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Sequence 532 from Patent WO0193902.
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da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida, Jr.N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Alwes, L.M.C., do Amaral, A.M., Bertolini, M.C., Camarayo, L.B.A., Camarotte, G., Cannavan, F., Cardozo, J., Crandozo, T., Crandozo, T., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Ferreira, R.C.C., Ferro, M.T., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Gruber, M. Kashi, L.T., Eeite Jr., R.N., Martine, R.C., Machado, M.A., Machara, A.M.B., M., Martins, E.C., Meidanis, J., Madelra, A.M.B., M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, W.R., Pereira Jr., H.A., Tamura, R.B., Teixeira, B.C., Tezza, R.L.D., Trindade dos Santos, M.A., Tamura, R.E., Teixeira, B.C., Tezza, R.L.D., Trindade dos Stantos, M., Tamura, R.E., Teixeira, R.F., Setubal, J.C. and Kitalima, J.P.
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2 da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monceiro vitorelio, C.B., Van Silva, W.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.B.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, E., Cicapha, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Sancos, J.R., Bl-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Perro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Guuber, A., Ratsuyama, A.M., Kishi, L.T., Leate Jr., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Machado, M.A., Maceira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Machado, M.A., Okura, V.K., Oliveira, W.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.P., Spinola, L.A.F., Takita, M.A., Tamura, R.B., Taaxeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, R.F., Setubal, J.C. and
13936 bp DNA linear BCT 23-NAY-2002 of 460 of the complete genome.
AE012163 AE08922
AE012163.1 GI:21171657
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'organism="Xanthomonas campestris pv. campestris str. ATCC
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Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade de
Sac Paulo, Av. Prof. Lineu Prestes 748, Sac Paulo, SP 05508-900,
Brazil
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                                                                                                                                                                                                                                                            Xanthomonas campestris pv. campestris str. ATCC 33913
Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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complement (422. .1654)
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Nature 417 (6887), 459-463 (2002)
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/gene="XCC0647"
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BOOMEALGMGSILSVARGSANRPRIIVLKWNGGGEARPYVLVGKGITFDTGGVNILKTO
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gene

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gene

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ocated using Blastx/Glimmer/Genemark*
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Query Match
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; 18 1 TGCGCCGATGCAGGGGG g ò

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Gaps

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13832 TGCGCAGATGCAGGGGG 13849

Search completed: July 2, 2004, 10:08:10 Job time : 636.732 secs

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July 2, 2004, 06:05:50 ; Search time 134.89 Seconds (without alignments) 566.887 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesequ2001as:\* genesequ2002s:\* genesequ2003as:\* genesequ2003as:\* genesequ2003cs:\* genesequ2003cs:\*

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SUMMARIES	ID	ACC48303	AAC80656	AAS09626	ABK46504	AAC80662	AAC80661	AAC80620	AAS09631	AAS09590	AAS09651	AAS09632	ABL35573	ABL35584	ABL35617	ABK46510	ABK46468	ABX46509	ACC48311	ACC48298	ACC48312	ACC48306	ACC48319	ACC83116
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	Length	C	19	19	19	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	90	20	20
de	Query	100.0	94.4	94.4	94.4	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	93.1	91.1	91.1	91.1	91.1
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Acc83117 D class C Acd01050 CpG D oli Add01059 CpG D oli Add1059 CpG D oli Abl35594 Immunosti Aac80602 Immunogen Aac80603 Immunogen Aac80663 Immunogen Aac90633 Immunogen Aac90631 Immunosti Abk46511 Immunosti Abk15587 Immunosti Abl35587 Immunosti Abl35652 Immunosti	ENTS			dendritic cell maturation.	cell; tumour; immunotherapy; vaccine; erapy; ss.		(especially G) or no base" (especially G) or no base"							tumor immunotherapy or as vaccines reat diseases such as cancer, precursor with a D type		a D type CpG oligodeoxynucleotide that is godeoxynucleotides (see ACC48294) of the
ACC83117 ACC83124 ADD01059 ABL35594 ABL35606 AAC80663 AAC806633 AAC80663 AAC80663 AAC80663 AAC80663 AAC80663 AAC80663 AAC80663 AAC80663 AAC80663 AAC8066 ABC8055 AAC806 AAC806 AAC	ALIGNMENTS	ВР.		for	endritic co		alifiers B any base s any base			_:	BOTVOOD NE	_		ritic cells for une system to to dendritic cell	English.	of oli
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invention. Mature dendritic cells are obtained by contacting a dendritic cell precursor, such as a monocyte, with such an oligodeoxymuclectide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to
                                                                                                                                                                                                                                                  produce activated T lymphocytes
      88888888888888888
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0; Gaps 7; Length 20; 0; Indels 'Match 100.0%; Score 18; DB Local Similarity 100.0%; Pred. No. 37; les 18; Conservative 0; Mismatches 3 TGCGCCGATGCAGGGGG 20 1 rececceargeagege 18 Query Match ò Q

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RESULT 2

AAC80656 standard; DNA; 19 BP

AAC80656;

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID WO:76.

CpG oligodeoxynucleotide, unmethylated, antigen-presenting cell, immunogenic; cytokine release, natural killer cell; NK cell activation; cell-mediated immune response; humoral response; sesponse; natibody production; immune response induction; vaccine; allergy, asthma; infection; baccerial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple selerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiatlergic; protozoacide; tuberculostatic; antiarthritic; antiathmatic; dermatological; phosphorothioate; ss.

Synthetic.

WO200061151-A2.

19-0CT-2000.

12-APR-2000; 2000WO-US009839.

99US-0128898P 12-APR-1999;

(KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERI/) VERTHBLYI D.

Verthelyi Ishii K, Klinman D,

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WPI; 2001-006880/01.

Novel oligonuclectides useful for the prevention and treatment of aliergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 35; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY-3'. The central CpG motif is unmerthylated, and the oligonucleotides optionally have phosphorothicate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targetting

cc agent, and a pharmaceutical composition comprising the oligonuclectide delivery complex. The oligonuclectides are able to induce either a cell-mediated (T-cell) response, with oligonuclectides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-RNMT-CpG-WNN-3' being able to induce a humoral response. It is thought that after administration, the oligonuclectide acts on antigan-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to exitvation of natural Xiller (NR) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliocrating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonuclectide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include exerma, allergic conditions which may be treated include viral, conditions, and the infections which may be treated include viral, conditions, and the infections which may be treated include viral, conditions, include approceased infections such as tuberculosis, ALDS, besterial, fungal and protozoal infections such as tuberculosis, ALDS, cleshmania and schistosomiasis. Immune response induction may also be exposure to an agent of biological warfare. An immunogenic CpG oligonuclectide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonuclectide is preferably administered to the host. The present sequence represents an immunogenic CpG oligodeoxynuclectide of the invention 

Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

0; Gaps 94.4%; Score 17; DB 4; Length 19; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 17; Conservative

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RESULT 3 AAS09626 ID AAS03

AAS09626 standard; DNA; 19

ВP

AAS09626;

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #76.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; bio-warfare; alfergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; autisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122. 

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

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AASO9551-AASO9662 represent oligodeoxynuclectides (ODN) of at least 10 nuclectides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The converse is different from another of the multiple CpG sequences. The converse is different from another of the multiple of sequences. The converse is different on inducing an immune response involving a cell activation, interferon gamma (IRN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma. Cc ancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for impreving the efficacy of vaccines cand other atopic conditions, for impreving the efficacy of vaccines cand other atopic conditions, for impreving the efficacy of vaccines cand other atopic conditions, for impreving the efficacy of vaccines cand other atopic conditions, for impreving the efficacy of vaccines cand other atopic conditions, for impreving the efficacy of vaccines corythearcuses and autoimmune system deficiency virus (HIV) and malaria, for treating immune system deficiency syndrome (AlDS), leishmania and multiple sclerosis, infections including Francisella, ecities and multiple sclerosis, infections including Prancisella, ecities and the efficacy of vaccines of symptoms resulting from exposure of bio-warfare agent, including Ebola,
                                                                                                                                        Oligodeoxynuclectides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Score 17; DB 4; Length 19; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
                            Verthelyi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pre
                                                                                                                                                                                                                                                                                            Claim 5; Page 39; 48pp; English.
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                            Ishii K,
                                                                                  WPI; 2001-442129/47.
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Best Local Similarity
                            Klinman D,
                                                                                                                                                                                                                                       sednences
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unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine; Paramyxoviridae; F protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.
                                                      Immunostimulatory unmethylated CpG oligodideoxynucleotide #94.
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10-AUG-2000; 2000US-0224011P. 01-SEP-2000; 2000US-0229307P. 09-AUG-2001; 2001WO-US041633

WO200211761-A2.

Synthetic

14-FEB-2002

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The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by quantine linked by phosphate bond) -oligodideoxymucleotidaes (DNBs). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have represents an oligodideoxymucleotide that can be used in the creation of the vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CpG oligodecoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimatopial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss.
                                                                                                   Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 6; Length 19;
Pred. No. 1.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Scc.
100.0%; Pred
0; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verthelyi D;
                                   Klinman DM;
                                                                                                                                                                           Claim 4; Page 9; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGCGCCGATGCAGGGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC80662 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0128898P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klinman D, Ishii K,
                                 Mond JJ, Prince G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISHI/) ISHII K.
(VERT/) VERTHELYI D.
                                                                   WPI; 2002-227118/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-006880/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KLIN/) KLINMAN D.
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Gaps

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Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 36; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxymucleotides (MAZC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5-NNN1-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NNNN-10-CpG-NN-10-CpG-NN-10-C CpG oligodeoxymucleotide of the invention

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

ö 91.1%; Score 16.4; DB 4; Length 20; 94.4%; Pred. No. 2.2e+02; live 0; Mismatches 1; Indels Local Similarity 94.4 tes 17; Conservative Query Match Best Loca Matches

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ठे g RESULT 6 AAC80661

AAC80661 standard; DNA; 20 BP.

AAC80661;

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

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Opd oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killar cell; MK cell activation; cell-mediated immuno response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; altergy, astehma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; luque erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent. antiarthritic; immune deficiency; biological warfare agent; cytostatic; an antimicrobial; antiallergic; protozoacide; tuberculostatic; antiasthmatic; dermatological; phosphorothioate; se. Verthelyi D; Claim 4; Page 36; 46pp; English. 12-APR-2000; 2000WO-US009839. 99US-0128898P. Klinman D, Ishii K, WPI; 2001-006880/01. (VERT/) VERTHELYI D. (KLIN/) KLINMAN D. WO200061151-A2. 12-APR-1999; 19-OCT-2000. Synthetic. (/IHSI) 

The invention relates to novel immunogenic CpG oligodeoxymucleotides (AACGORDI-CBOTA). The oligomucleotide are at least 10 bases long and comprise one of the generic sequences \$\(\circ\)-NNNT-CpG-WNNY-1 or \$\(\circ\)-X-Y-CpG-XY-CCC (Comprise one of the generic sequences \$\(\circ\)-NNNT-CpG-WNNY-1 or \$\(\circ\)-X-Y-CpG-XY-CCC (Comprise one of the generic sequences \$\(\circ\)-NNT-CpG-WNNY-1 or \$\(\circ\)-X-Y-CpG-XY-CCC (Comprising an oligomucleotide delivery complex. The oligomucleotides which make them more resistant to degradation. The inventional also relates to an oligomucleotide delivery complex. The oligomucleotides are able to induce either a cell-mediated (T-cell) response or a humoral [8-cell, antibody) response, with oligomucleotides of the sequence 5'-RNY-CpG-RY-3' being able to induce a humoral response. It is thought that after administration, the oligomucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytofines, leading to activation of natural killer (NK) cells. A cell-mediated or calls and an allergic reaction (preferably asthma), or an infection, and an immune response is useful for treating, preventing or meliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligomucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infections, and the infections which may be treated include erzema, allergic conditions which may be treated include erzema, allergic conditions

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20; Best Local Similarity 94.4%; Pred. No. 2.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels

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Gaps

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1 TGCGCCGATGCAGGGGG 18

Query Match

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TGCGTCGATGCAGGGGG 20
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AAC80620 standard; DNA; 20 BP AAC80620 

AAC80620;

Immunogenic CpG oligodeoxynucleotide, SBQ ID NO:40.

(first entry)

14-FEB-2001

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunoganic; cytoxine release; natural killer cell; ix cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; natibody production; immune response induction; vaccine; altergy; sathma; infection; bacterial; viral; fungal; protozoal; parastic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; amtimune deficiency; bloodgatal warfare agent; cytostatic, antiarthritic; antimiatorobial; antiallergic; protozoacide; tuberculostatic; antiathritic; antiasthmatic; dermatological; phosphorothioate; ss.

WO200061151-A2.

19-OCT-2000

12-APR-2000; 2000WO-US009839.

99US-0128898P. 12-APR-1999;

ISHI/) ISHII K. VERI/) VERTHELYI D. KLIN/) KLINMAN D.

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English

The invention relates to novel immunogenic CpG oligodecxynuclectides

(AAC80581-C80723). The oligonuclectide are at least 10 bases long and

comprise one of the generic sequences 5. "ANNT-"CpG-"NNN-3' or 5. RY-CpG-RY

-3'. The central CpG motif is unmethylated, and the oligonuclectides

comprise one of the generic sequences 5. "ANNT-"CpG-"RY-CpG-"RY

comprising an oligonuclectide of the invention and a targetting

agent, and a pharmaceutical composition comprising the oligonuclectide

complex comprising an oligonuclectides are able to induce either a cell
complex pomplex. The oligonuclectides are able to induce either a cell
complex pomplex. The oligonuclectides are able to induce either a cell
mediated (T-cell) response or a humoral [-cell, antibody) response, with

coligonuclectides of the sequence 5'-RY-CpG-RY-3' being able to induce a

coll-mediated response, and those of the sequence 5'-RNT-CpG-RNNN-3'

coll-mediated or induce a humoral response. It is thought that after

coll-mediated or induce a numeral response. It is thought that after

defining able to induce a numeral response. It is thought then release cytokines,

coll-mediated or immune response is useful for treating, preventing or

ameliorating an allergic reaction (preferably asthma), or an infection,

where an immunogenic CpG oligonuclectide is administered either alone or

conditions with an anti-allergenic agent or anti-infectious agent.

The allergic conditions which may be treated include eczema, allergic

conditions, and the infections which may be treated include viral,

ö bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and sofistosomisais. Immune response induction may also be used in the treatment of an autoimmune disorder [e.g., lupus erythematosus, rheumatoid arthritis and multiple solerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligomucleotide, either alone or in combination with an anti-cancer along each is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligomucleotide is preferably administered to any administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention Gaps .. Score 16.4; DB 4; Length 20; Pred. No. 2.2e+02; 0; Mismatches 1; Indels Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other; ö 1 TGCGCCGATGCAGGGGG 18 94.48; Local Similarity 94.4 Query Match Best Loca Matches à

20 3 TGCGTCGATGCAGGGGGG a

AAS09631 standard; DNA; 20

BP.

AAS09631;

(first entry) 26-SEP-2001 Immunoreactive CpG sequence-containing oligonucleotide #81.

CpG sequence; immune response; non-B cell activation; interferon gamma; therageutic; allergy; asthma, cancer; autoimmune disorder; infection; therageutic; allergy; asthma, cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Prancisella; lupus erythematosus; rhematoid arthritis; multiple sclerosis; schiatosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122,

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

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Verthelyi

Ishii K,

Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences

Claim 5; Page 40; 48pp; English.

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 mucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from annother of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, preferably interferon

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cell activation, antibody and interleukin-6 production in a host, for cell activation, antibody and interleukin-6 production in a host, for creating, preventing or alleggic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection cc a symptom resulting from asposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is compared in antisense therapy. The ODN are useful for treating, preventing or cc analiorating allergic reactions, including ecram, allergic rhintis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines capainst hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus creating immune diseases such as rheumatoid arthritis and cmultiple sclerosis, infections including Francisella, solistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AlDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, XX Anthrax and Listeria
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Score 16.4; DB 4; Length 20; Pred. No. 2.2e+02; Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other; 0; Mismatches 18 94.48; 1 TGCGCCGATGCAGGGGG 17; Conservative Query Match Best Local Similarity Matches à g

20 3 TGCGTCGATGCAGGGGG

RESULT 9

AAS09590 standard; DNA; 20 BP. AAS09590

AAS09590;

(first entry) 26-SEP-2001

Immunoreactive CpG sequence-containing oligonucleotide #40.

ifN-gamma; humoral; antibody production; interleuxin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; blo-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lugua erythemacrosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss. sequence; immune response; non-B cell activation; interferon

Synthetic

WO200151500-A1.

19-JUL-2001

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Klinman D, Ishii K, Verthelyi

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences 

Claim 5; Page 33; 48pp; English

conditions to inducing an immune response, preferably a cellcondition inducing an immune response, preferably a cellcondition are response, involving non-B cell activation, interferon
cell activation, antibody and interleukin-6 production in a host, for
cell activation, artibody and interleukin-6 production in a host, for
cell activation or ameliorating an allergic reaction, e.g. asthma,
cencer, e.g. solid tumour cancer, a disease associated with the immune
system e.g. autoimmune disorder or an immune system deficiency, infection
con a symptom response improves the efficacy of a vaccine and is
induction of immune response improves the efficacy of a vaccine and is
cused in antisense therapy. The ODN are useful for treating, preventing or
coryza, hay fever, bronchial asthma, urticaria (hives), food allergic and other atopic conditions, for improving the efficiency virus (HIV) and
coryza, heytever, bronchial asthma, urticaria (hives), food allergics
adainst hepatitis A, B and C, human immundefficiency virus (HIV) and
coryza, heytevering immune system deficiencies, e.g. lugus
corythematosus and autoimmune diseases such as rheumatoid arthritis and
multiple sclerosis, infections including Francisella, schistosomiasis,
cuberculosis, acquired immunodeficiency syndrome (ALDS), Leishmania and
symptoms resulting from exposure of bio-warfare agent, including Ebola, AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. ODN are useful for inducing an immune response, preferably a cell-Anthrax and Listeria 88888888888888888888888888888

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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1; Indels

Gaps 6 91.1%; Score 16.4; DB 4; Length 20; 94.4%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels Best Local Similarity 94.4%; Matches 17; Conservative Query Match Matches

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δ ద RESULT 10 AAS09651

AAS09651 standard; DNA; 20 BP.

26-SEP-2001 (first entry)

AAS09651;

Immunoreactive CpG sequence-containing oligonucleotide #101.

CpG sequence, immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001, 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi Ishii K, Klinman D,

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WPI; 2001-442129/47.

Oligodeoxymucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms 

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AAS09551-AAS09662 represent oligodeoxymuclectides (ODN) of at least 10 nuclectides comprising multiple CpG sequences, where one of the CpG sequences. Inclease in a different from another of the multiple CpG sequences. The CDN are useful for inducing an immune response, preferably a cell-condition of a first of the multiple CpG sequences. The CDN are useful for inducing an immune response involving B cell activation, interferon companies of the multiple cpd and interleukin 6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthmaccancer, e.g. solid tumnour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to blo-warfare agent in a human. The core of induction of immune response improves the efficacy of a vaccine and is useful to intisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines of against hepatitis A, B and C, human immunodeficiency virus (HIV) and coryza, hay fever, bronchial asthma immunodeficiency virus (HIV) and coryza, hay fever, bronchial asthma immunodeficiency virus (HIV) and coryza, hay fever, bronchial asthma immunodeficiency wines (HIV) and coryza, hay and utchimune system deficiency virus (HIV) and malaria, for treating immuno diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), isosomiasis, anther when and itserial is manual asthma and allergic is and multiple sclerosis, infections including francisella, schistosomiasis, anther and itserial is and multiple sclerosis, infections including each as the including sclerosis, infections including each as the afficact.
resulting from exposure to bio-warfare agents, comprise multiple CpG
                                                                                                                 Claim 5; Page 44; 48pp; English
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Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

91.1%; Score 16.4; DB 4; Length 20; 94.4%; Pred. No. 2.2e+02; i; Indels Mismatches . . 18 20 TGCACCGATGCAGGGGGG 1 TGCGCCGATGCAGGGGG Conservative Query Match Best Local Similarity Matches 17; Conserv 8 용

RESULT 11 AAS09632

AAS09632 standard; DNA; 20 BP. AAS09632; 

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #82.

CpG sequence; immune response; non-B cell activation; interferon gamma; then gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001

12-JAN-2001; 2001WO-US001122

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG segnences

Claim 5; Page 40; 48pp; English.

AMBOUSTATEMANDEA FURTHEREBUL OLIGOROGES (UNIV) OI ST LEAST IN UNIVERSITY AMBOUSTATEMANDEA FURTHEREBUL OLIGORIGES COMPRIBING MULLIPLE CDG SEQUENCES. THE OND AIR UNEFLOOD SEQUENCES. THE OND AIR USEFUL FOR INTERPRETABLY A CELL.

CON AIR USEFUL FOR INDIVIDUA CONTROL SEQUENCES. THE OND AIR USEFUL SET SEQUENCES. THE OND AIR USEFUL SET SEQUENCES. THE OFFICE SEQUENCES. THE OFFICE SEQUENCES. THE OFFICE SEQUENCES. THE SEQUENCE IN AIR USEFUL SEQUENCES AND AIR USEFUL SEQUENCES. THE SEQUENCES OF SECRET SEQUENCES. THE SEQUENCES. OF SEQUENCES. AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least Anthrax and Listeria

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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Gaps .. o

Gaps ö Score 16.4; DB 4; Length 20; Pred. No. 2.2e+02; 0; Mismatches 1; Indels 0 Query Match
Best Local Similarity 94.40,
-1-68 17; Conservative

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ठ G ABL35573 standard; DNA; 20 BP. ABL35573; 

Immunostimulatory oligonucleotide SEQ ID NO: 499.

(first entry)

04-APR-2002

DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; se.

Synthetic.

Location/Qualifiers misc RNA

1..20 /\*tag= //ord= "optionally thymidine is replaced by uracil to /note= "optionally thymidine is linked to at form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

WC200193902-A2.

13-DEC-2001.

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RESULT 14
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                                                                                                                                                                                                          The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines, it can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic thinitis, hay fever or food allergies), Lywe disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                         New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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/note= "optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
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Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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            07-JUN-2001; 2001WO-US018276.
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                                 G7-JUN-2000; 2000US-0209797P
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                Klinman
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                                                         (BIOS-) BIOSYNEXUS INC.
                                                                                                      WPI; 2002-130570/17.
                                                                                Flora M,
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                                                                                                                                                                                                                                                                                                                                                       the invention
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misc_RNA
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                                                                                Mond JJ,
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytckines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of

    .20
    /*tag= a
    /note="optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

                                                                                                                                                                                                                                                                               New immunostimulatory compositions comprising RNA/DNA hybrid obliganceLectides, useful for enhancing an immune response or inducing cytckines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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                                                                                                                                         Klinman DM
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07-JUN-2000; 2000US-0209797P
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                                                                      (BIOS-) BIOSYNEXUS INC.
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                                                                                                                                             Flora M,
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Matches
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linked by phosphate bond-oligodideoxymucleotides.

Claim 4; Page 9; 30pp; English

Klinman DM;

Flora M,

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New immunostimulatory compositions comprising RNA/DNA hybrid obligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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                                (BIOS-) BIOSYNEXUS INC
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(first entry)

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The present invention relates to an immunostimulatory composition, which comprises at least one oligonuclectide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
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Pred. No. 2.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
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Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae P protein, and cytosine followed by guanine

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED

09-AUG-2001; 2001WO-US041633. 10-AUG-2000; 2000US-0224011P. 01-SEP-2000; 2000US-0229307P.

WO200211761-A2.

14-FEB-2002

Klinman DM;

Prince G,

Mond JJ,

WPI; 2002-227118/28

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                                                                             The invention describes a vaccine comprising one or more epitopes of a paramyxoviridae P protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodideoxynucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV); the primary cause of viral bronchlolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premeture, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Job time : 134.89 secs
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APPLICANT: BASBAUM, Carol
APPLICANT: BASBAUM, Carol
APPLICANT: GALLUC, Marianne
APPLICANT: GALLUC, Marianne
APPLICANT: GALLUC, Marianne
APPLICANT: GEBREMICHAEL, Assefa
TITLE OF INVENTION: MCIN GENE EXPRESSION
FILE REFRENCE: UCSF-012/03US
CURRENT FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 09/248,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-248-571-2
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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 41.0, Appli
Sequence 41.0, Appli
Sequence 10, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 2220, Appli
Sequence 2220, Appli
Sequence 2220, Appli
Sequence 2220, Appli
Sequence 2230, Appli
Sequence 2380, Appli
Sequence 2381, 
                                                                                                                                             2, 2004, 08:09:30 ; Search time 28.2073 Seconds (without alignments) 354.132 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2 6/ptcdata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2 6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptcdata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PcTUS COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-175-014-1
US-09-175-014-1
US-09-328-475C-59
US-09-328-475C-59
US-09-252-991A-4643
US-09-252-991A-4643
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2220
US-09-252-991A-2580
US-09-252-991A-2580
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US-09-252-991A-2537
US-09-659-845A-106
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US-09-553-736-2
US-08-111-939-1
US-09-077-354B-3
US-09-103-840A-2
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                  tgcgccgatgcagggggg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
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18
1 tgcgccgatgcaggg
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Match 1
                                                                                                                                                July
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Maximum DB
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Perfect :
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Sequence 2, Application US/09248571
Fatent No. 6136539
GENERAL INFORMATION:
APPLICANT BASBAUM, CARCL
APPLICANT GALLUP, WARIANNE
APPLICANT GALLUP, MARIANNE
APPLICANT GALLUP, MARIANNE
APPLICANT GENERAL ASSERA
APPLICANT GENERAL HEIN
TITLE OF INVENTION COMPOSITIONS AND METHODS FOR INHIBITION OF MUCIN
TITLE OF INVENTION COMPOSITIONS AND METHODS FOR INHIBITION OF MUCIN
TITLE OF INVENTION UCONSTRUCTOR AND METHODS FOR INHIBITION OF MUCIN
TITLE OF INVENTION UCONSTRUCTOR AND THE REPERSOR
TITLE OF INVENTION DUMBER: US/09/248,571
CURRENT FILING DATE: 1999-02-11
MUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENT VET. 2.0
SOFTWARE: PATENT VET. 2.0
SOFTWARE: PATENT VET. 2.0
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         9670, Ap
17623, Ap
9630, Ap
121357, Ap
7532, Ap
9228, Ap
11322, A
111322, A
111028, Ap
9710, Ap
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                                 Sequence Seq
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Pred. No. 2.3e+02;
); Mismatches 2; Indels
US-09-252-991A-9670
US-09-489-038A-7023
US-09-252-991A-1446-9
US-09-252-991A-11367
US-09-252-991A-11367
US-09-252-991A-7811
US-09-252-991A-7811
US-09-252-991A-7812
US-09-252-991A-1132
US-09-252-991A-1132
US-09-252-991A-11028
US-09-252-991A-11028
US-09-252-991A-9145
US-09-252-991A-9145
US-09-252-991A-910
US-09-252-991A-910
US-09-252-991A-910
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
US-09-252-991A-010
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Patent No. 6440672
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Best Local Similarity 88.9
Matches 16, Conservative
      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2
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: 10380 base pairs
nucleic acid
BDNESS: single
                                                                      Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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2115..2262
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3056..3202
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990..1372
                      69..3452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
PEATURE:
NAME/KEY:
                      ; LOCATION:
US-08-111-939-1
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NAME/KEY:
LOCATION:
     NAME/KEY:
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                                                                                                                                                                                                                                   Gaps
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Patent No. 5460951
GENERAL INFORMATION:
APPLICANT: Kawai, Shinji
APPLICANT: Takeshita, Sunao
APPLICANT: Awan, Bone
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ADBRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                            Score 14.8; DB 4; Length 3358;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITX:
STATE: D.C.
CUNTAY. USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/111,939
TITTING DATE: 26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02481.1321-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
PRIOR FILING DATE: 1999-02-11
RIOR APPLICATION NUMBER: US 60/074,398
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 3358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324033/92
PRIOR APPLICATION NUMBER: JP 230029/92
PLING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     999 TGCACCCATGCAGGGGG 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: FORMAI, DAVIG S.
REGISTRATION NUMBER: 33,694
REFREENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
                                                                                                                                                                                                                                                                 1 TGCGCCGATGCAGGGGG 18
                                                                                                                                                                                          Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUEDICE CHARACTERISTICS: LENGTH: 3728 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-553-736-2
                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-111-939-1/c
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Score 14.8; DB 1; Length 3728;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 105/09/077,354B
FILING DATE: 22-APRIL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00747
FILING DATE: 22-APRIL-1996
ATTORNEY/AGENT INFORMATION:
NAME: PORALLSKY, ANN R.
REGISTRATION NUMBER: 12416
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW YORK
COUNTRY: UNITED STATES
ZIP: 115:0
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DX
                                                                                                                     3093 receceeracradeede 3076
                                                                                1 TGCGCCGATGCAGGGGG 18
    82.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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US-09-103-840A-2

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US-09-252-991A-4236/C

Sequence 4226, Application US/09252991A

Sequence 4226, Application US/09252991A

Sequence 4226, Application US/09252991A

Patent No. 6551798

TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS

TITLE OF INVENTION: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27

SEQ ID NO 4236

LENGTH: 648
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERRNE: 24366-250007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SUPTERN FILING DATE: 1998-06-24
SOFTWARE PACENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4411529;
                                              Score 14.8; DB 3; Length 4403765;
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 14.4; DB 4; Length 648; larity 93.8%; Pred. No. 3.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
82.2%; Score 14.8; I
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                      173979 receccarrecaecece 173962
                                                                                                                                                                                                                                                     RESULT 7
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INPORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173810 receccaricalecaececci 173793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4236
                                                                                                                                          1 TGCGCCGATGCAGGGGG 18
                                                   82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 TGCGCCGAGGCAGGGG 248
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                                                                      Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 15; Conserv
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Fatent No. 6294328
GENERAL INFORMATION
APPLICANT: FIEISCHMAN, Robert D.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFREENCE: 24566-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 2
LENGTH: 4403765
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, L, c or g
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09144085
Fatent No. 628099
GENERAL INFORMATION:
APPLICANT: Gustaffsson, Claes
APPLICANT: Betlach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Allien, Bryan
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: THERREPC
TITLE OF INVENTION: 19062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT FILING DATE: 1998-08-31
FARLIER APPLICATION NUMBER: 09/010,809
EARLIER PILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 3
                                                                                                                                                                                        Gaps
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                                                                                                                                     Score 14.8; DB 3; Length 10380;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.8; DB 3; Length 33529;
Pred. No. 2.18+02;
0; Mismatches 2: TrAmle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30209 rececadarecadedese 30226
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CRGANISM: Sorangium cellulosum
US-09-144-085-3
                                                                                                                                     Watch B2.2%;
Local Similarity 88.9%;
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%;
88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
                                           exon 6
7745..8955
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US-09-103-840A-2/C
LOCATION:
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 33529
                                         ; NAME/KEY:
; LOCATION:
US-09-077-354B-3
                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-144-085-3
                                                                                                                                   Query Match
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Matches
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JS-09-175-014-1

FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(753)

US-09-175-014-1

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Sequence 4168, Application US/09252991A
Sequence 4168, Application US/09252991A
Sequence 4168, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENCE: RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 4168
LENGTH: 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4643, Application US/09252991A

Patent No. 6551795

REBERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINGS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252, 991A

PRIOR APPLICATION NUMBER: US 60/074,788
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APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

APPLICANT: Steinmann, Kathleen E.

TITLB OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

FILE REFERENCE: 1532.002/200130.463

CURRENT PPLICATION NUMBER: US/09/328,475C

CURRENT PILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 59

LENDTH: 1024

TYPE: DATA
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Pred. No. 3.6e+02;
0; Mismatches 3;
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93.8%; Pred. No. 3.6e+02;
clive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 TGCGCCGNTACAGGGNGG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
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Best Local Similarity 83.3%
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Best Local Similarity 93.81
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-252-991A-4168/c
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US-09-252-991A-4643
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US-09-252-991A-4440

US-09-252-991A-4440

Sequence 4440, Application US/09252991A

Fatent No. 6551795

GENUERAL INFORMATION:

APPLICANTON: NUCLBIC ACID AND AND AND AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

FRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

SEQ ID NO 4440

LENGTH: 771

THE APPLICATION NUMBER: US 60/094,190

BRIOR FILING DATE: 1998-07-27

SEQ ID NO 4440
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80.0%; Score 14.4; DB 3;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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80.0%; Score 14.4; DB 4;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                               Sequence 1, Application US/09175014
Fatent No. 6761802
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: Jiang, Xinhe
APPLICANT: Jiang, Xinhe
APPLICANT: MoDevitt, Damien
ITLE OF INVERTION: ups (ugc)
FILE REFERENCE: GM10171
CURRENT APPLICATION NUMBER: US/09/175,014
CURRENT PILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NOT
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US-09-328-475C-59/C
Sequence 59, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddi
APPLICANT: Endege, Wilson O.
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US-09-252-991A-4440

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TYPE: DNA

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Sequence 1, Application US/09578441

Patent No. 656297

GRERAL INFORMATION:
APPLICANT: Omasa, Takeshi
APPLICANT: Omasa, Takeshi
APPLICANT: Omasa, Takeshi
APPLICANT: Mantalaria, Athanassios
APPLICANT: Applicant and a sequence 1
APPLICANT: Tsai, Ying-Chuech
TITLE OF INVENTION: HUMAN HEMB-REGULATED INITIATION FACTOR 2.ALPHA KINASE
FILE REFERENCE: 176/60571
CURRENT APPLICATION NUMBER: US/09/578,441
CURRENT APPLICATION NUMBER: 06/0578,713
PRIOR APPLICATION NUMBER: 60/135,713
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 5
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Parent No. 6638721

GENERAL INFORMATION:
APPLICANT: Mayers, Rachel
APPLICANT: Majliamson, Mark
ITILE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
ITILE OF INVENTION: Therefor
ITILE OF INVENTION: Therefor
FILE REFERENCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/09, 875
CURRENT FILING DATE: 2000-00-11
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGER: 2870
TYPE: DNA
ORGANISM: Homo sapiens
NAMENTEN:
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80.0%; Score 14.4; DB 4; Length 1503;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
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80.0%; Score 14.4; DB 4; Length 2870;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0.
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; WINMER OF SEQ ID NOS: 33142
; SEQ ID NO 4643
; TYPE: DNA
; ORGANIGM: Peeudomonas aeruginosa
US-09-252-991A-4643
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; LOCATION: (114)...(2000)
US-09-799-875-16
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US-09-578-441-1
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July 2, 2004, 08:11:05; Search time 138.732 Seconds (without alignments) 625.926 Million cell updates/sec
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Sequence 499
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Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-666-022-6
US-10-194-035-76
US-10-068-160-16
US-09-874-991C-510
US-09-874-991C-543
US-10-068-160-7
US-10-068-160-7
US-10-108-160-7
US-10-194-035-82
US-10-194-035-82
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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Sequence 16, Appl Sequence 520, App Sequence 532, Appl Sequence 22, Appl	iequence 239, equence 506, equence 513, equence 146, equence 151, equence 12, equence 12, equence 496, equence 502, equence 502, equence 502, equence 503, equence 503, equence 534, equence 534, equence 534, equence 534,	Sequence 541, App Sequence 546, App Sequence 550, App
-10-66 -09-87 -09-87 -10-19	-10 -257 -8264-2 -10 -437 -9624-2 -10 -437 -9624-2 -10 -874 -991C-5 -10 -08 -160 -12 -10 -068 -160 -12 -10 -874 -991C-5 -09 -874 -991C-5	US-09-874-991C-541 US-09-874-991C-546 US-09-874-991C-550
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US-10-06-16

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Sequence 18, Application US/10068160

Sequence 18, Application US/10068160

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Sequence 18, Application WS.

Sequence 18, Application WS.

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OP AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: ISHII, Kennis

APPLICANT: WERTHELYI. Daniela

APPLICANT: WERTHELYI. Daniela

TITLE OF INVERTION OLIGODEXXNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

TITLE REPREMENCE: 4039-61399

CURRENT FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOFTWARE: PAPLICATION NUMBER: 60/128,898

PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 18

IRROTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

SEQ ID NO 18

TYPE: DNA

ORGANISM: Artificial Sequence

SEQ ID NO 18

TYPE: DNA

OTHER INFORMATION: Oligonucleotide

US-10-068-160-18

OTHER INCOMENTATION: Oligonucleotide

US-10-068-160-18

ONE OF SECONDER THE OLIGONUCLEOTIDE

DD 1 TGGCCCANGCAGGGGGG 18

DD 1 TGGCCCANGCAGGGGG 18
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RESULT 2 US-10-666-022-6

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Sequence 16, Application US/10068160
) Sequence 16, Application US/10068160
) Publication No. US20030060440A1
) GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: TELINMAN, Dennie
APPLICANT: SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: WERTHELYI, Dennie
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXINUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TILE REPREMENCE: 4239-61999
CURRENT PELLING DATE: 2002-02-06
CURRENT PELLING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SPETION FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SSEQ ID NO IS
LENGTH: 18
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US-09-874-991C-499
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APPLICANT: FLORA, MICHARL
APPLICANT: FLORA, MICHARL
APPLICANT: KLINAN, DENNIS M.
ITILE OF INVENTION: INMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 16.4; DB 13; Length 20; larity 94.4%; Pred. No. 1.46+02; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.4e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 499, Application US/09874991C Publication No. US20040052763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide US-10-068-160-16
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Best Local Similarity 94.4%;
Matches 17; Conservative
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ORGANISM: Artificial Sequence
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hes 17; Conserv
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US-09-874-991C-499
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Best Local S
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Sequence 76, Application US/10194035

Publication Vo. USZ0030144229A1

SERERAL INPORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: USETHERNY OF THE DEPARTMENT OF USE TO INDUCE AN IMMUNE RESPONSE

ITLE OF INVENTION: OLIGODEOXYMUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

TITLE OF INVENTION NUMBER: US/10/194,035

CURRENT FILING DATE: 2002-07-12

PRIOR PELLORYICON NUMBER: US/0/176,115

PRIOR PELLORYICON NUMBER: US 60/176,115

PRIOR APPLICATION NUMBER: US 60/176,115

PRIOR SEQ ID NOS: 119

NUMBER OF SEQ ID NOS: 119
                                        GENERAL INFORMATION NO.

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Werthelyi, Danish
APPLICANT: Verthelyi, Danish
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REFERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-18
SOFTWARE: Patentin Version 3.1
SSEQ ID NO 6
LENGTH: 20
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US-10-194-035-76
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LOCATION: (1)...(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
Application US/10666022
No. US20040105872A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserv
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RESULT 6 US-09-874-991C-510 Sequence 510, Application US/09874991C Publication No. US20040052763A1

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US-10-194-035-40
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APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Kn
APPLICANT: USHII, Kn
APPLICANT: VERTHELYI, Daniela
ITILE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
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US-09-874-991C-510
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APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: KICHAMN, DENNES M.
TITLE OF INVENTION: IMMUROSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT PILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
SOFTWARE: PACENTIN VEY: 2.1
SEQ ID NO 543
LENGTH: 20
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                                   APPLICANT: FEORA, MICHAEL
APPLICANT: FEORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVESTION: IMMONSCIPMILATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT PALICATION NUMBER: US/09/874,991C
CURRENT PILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PATENTIN Ver. 2.1
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.larity 94.4%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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Pred. No. 1.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 94.4%;
Matches 17; Conservative
                    APPLICANT: MOND, JAMES J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               SEQ ID NO 510
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Sequence 37, Application US/10068160
Publication No. US20030060440A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: RLINMAN, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: USRTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLECTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE FILE REFERENCE: 4219-6199
GURRENT APPLICATION NUMBER: US/10/068,160
GURRENT PILLING DATE: 2002-02-06
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Publication No. US20030144229A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINNAN, Dennis
APPLICANT: KLINNAN, Dennis
APPLICANT: USHTI, KD
APPLICANT: USHTI, VD
APPLICANT: US
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Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1;
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR PILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 20
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PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 20
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Sequence 4. Application US/10666022
Sequence 4. Application US/10666022
Eublication No. US20040105872A1
Eublication No. US20040105872A1
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Klinman, Dennis M. APPLICANT: Verthely1, Daniela
TITLE OF INVENTION: WETHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REPERENCE: 4239-66899
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: THE GOVERNMENT OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KENEMAN, Dennis
APPLICANT: ISHLI, Ken
APPLICANT: VERTHELYI, Daniela
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA US-10-194-035-82
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Pred. No. 1.4e+02;
0; Mismatches 1;
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CURRENT PILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: ECT/US01/01122
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
LENGTH: 20
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 82
LENGTH: 20
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o. US20030144229A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity 94.4;
Matches 17; Conservative
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US-10-666-022-4
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Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT:
KLINMAN, Dennis
APPLICANT:
SERTIFICANT:
ISHII, Ken
APPLICANT:
ISHII, Ken
APPLICANT:
GURRENT FILING DATE:
2002-07-12
PRIOR APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE:
2002-07-12
PRIOR APPLICATION NUMBER: US/01/1012
PRIOR APPLICATION NUMBER: US/01/1012
PRIOR APPLICATION NUMBER: US/01/1012
PRIOR APPLICATION NUMBER: US/01/10112
PRIOR APPLICATION NUMBER: US/01/10112
PRIOR APPLICATION NUMBER: US/01/10112
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Publication No. US20030144229A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: THE GOVERNMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINAM, Dennis
APPLICANT: KLINAM, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ren
APPLICANT: UNIVENTION: OLIGODROXXNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REPERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
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  APPLICATION NUMBER: PCT/USO1/01122
FILING DATE: 2001-07-19
                                                 PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 40
LENGTH: 20
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 20
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US-10-666-022-16

Sequence 16, Application US/10666022

Sequence 16, Application Wo. US20040105872A1

Publication No. US20040105872A1

Sequence 16, Application No. US20040105872A1

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Kinman, Dennis M.

APPLICANT: Verthely, Daniela

TITLE OF INVENTION: METEOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED

TITLE OF INVENTION: WIBER: US 001-09-1

TITLE OF INVENTION: WIBER: US 001-09-1

FILE REFERENCE: 423-966899

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: US 60/411,944

PRIOR FILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 181

SSOTUMMER: Patentin version 3.1

LENGTH. 20
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CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 20
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ORGANISM: Artificial Sequence
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// OTHER INFORMATION: synthetic US-10-666-022-16
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Search completed: July 2, 2004, 13:58:26 Job time: 139.732 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ñ	Sequ	Se	Sed	J C	Sear	Sequ	O C		נט נ	S)	OJ C	<i>1</i> 3 U.	S	0, 0	Sequenc	တဲ့	Ω,		S	01 0	လ လ	S		) (J)	S		ŝ	Sequenc		Sequenc	Sequenc	υ o	quenc	Se		-	-	linear PAT 28-AUG-2001					e an immune response	Human Services (US)
SUMMARIES	ID	AX194432	AX194434	AX194437	AX194438	AA10443	AX352198	AX352209	AX352242	AX465382 BY465384	AX465387	AX465388	AX465393	AX465422 AX816067	AX352204	AX352248	AX352219 AX352233	AX352237	AX352225	AX35250 AX352167	AX194453	AX194473	AX465423	AX194440	AX194481. AX194482	AX194500	AX194501	AX194504	AX194507	AX352202	AX352203	AX352214	AX352246	AX352247	AX465431	AX465432	ALIGNMENTS			20 bp	ent Montolo	8800			and Verthely	3 2
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PAT 28-AUG-2001

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Klinman,D., Ishii,K. and Verthelyi,D.
Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 38 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol type="unassigned DNA"
/dD_xref="taxon:32630"
/noce="Synthetic DNA"
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Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches
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Sequence 38 from Patent WO0151500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Klinman, D., Ishii, K. and Verthelyi, D. Oligodeoxyrucleotide and its use to induce an immune response Patent: WO 01515/00, 34 19-JUL-2001; Secretary of the Department of Health and Human Services (US)
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Sequence 34 from Patent WO0151500
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PAT 28-AUG-2001
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 43 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Synthetic DNA"
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Sequence 43 from Patent WC0151500.
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Vaccine against RSV
Vaccine against RSV
Batent: W 0211761-A 50 14-FEB-2002;
HENRY W. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 16;
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                               Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 505 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 538 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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/note="Synthetic HDR"
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/note="Synthetic HDR"

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    /organism="synthetic construct"

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches
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Mond,J.J., Flora,M. and Klinman,D.M.
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Seguence 538 from Patent WO0193902.
AX352242
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Sequence 50 from Patent W00211761.
AX465382
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Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 72 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 494 13-DEC-2001;
Blosynexus Incorporated (US)
Location/Qualifiers
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/noTe="Synthetic HDR"
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/mol Lype="unassigned DNA"
/db xref="taxon:32630"
/noFe="Synthetic DNA"
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Sequence 494 from Patent WO0193902.
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Seguence 72 from Patent WO0151500.
AX194472
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Vaccine against RSV
Patent: WO 0211761-A 56 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY MEDICINE (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mond,J.J., Prince,G. and Klinman,D.M.
Vaccine against RSV
Vaccine against RSV
Parent: W0 0211761-A 61 14-PEB-2002,
PERRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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/organism="synthetic construct"
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/organism="synthetic construct"
/organism="synthetic construct"
/organism="synthetic blag."
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
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      Mismatches
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Sequence 56 from Patent WO0211761.
AX465388
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Sequence 61 from Patent WO0211761.
AX465393
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AX465393
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Vaccine against RSV
Barent: WO 0211761-A 52 14-PEB-2002;
FERRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mond, J.J., Prince, G. and Klinman, D.M.
Vaccine against RSV
Vaccine against RSV
Barent: MO 0211761-A 55 14-PEB-2002;
HENRY W. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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/onl_type="unassigned DNA"
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/db xref="taxon:33630"
/note="Synthetic oligonucleotide"
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Seguence 52 from Patent WO0211761.
AX465384
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Sequence 55 from Patent WO0211761.
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AX465384
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Gaps

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linear PAT 16-JUL-2002
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Vaccine against RSV
Vaccine against RSV
Barent: WO 0211761-A 90 14-FEB-2002;
FERRY W. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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/note="Synthetic oligonucleotide"
                                     DNA
                            20 bp
Sequence 90 from Patent WO0211761.
AX465422
AX465422.1 GI:21899785
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                                                                                                          synthetic construct
synthetic construct
artificial sequences.
RESULT 15
AX465422
LOCUS
DEFINITION
ACCESSION
VERNORDS
SOURCE
ORGANISM
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AUTHORS
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Search completed: July 2, 2004, 10:07:54 Job time : 705.146 secs

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0; Gaps

Query Match
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels

ORIGIN

OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Scarched:	GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: July 2, 2004, 06:05:50; Search time 149.878 Seconds  (without alignments)  566.887 Million cell updates/sec  Title: US-10-068-160-1  Perfect score: 20 Sequence: 1 ggtgcatcgatggaggggggggggggggerence: 1 ggtgcatcgatggaggggggggggggggggggggggggg
Minimum DB seq le	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn20028;\* geneseqn2003as;\* geneseqn2003bs;\* geneseqn2003cs;\* geneseqn2004s:\* 4.0.67.89.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aac80617 Immunogen Aac80613 Immunogen Aac80623 Immunogen Aac09582 Immunorea Aac09587 Immunorea Aac09587 Immunorea Aac09587 Immunorea Aac80652 Immunogen Aac80614 Immunogen Aac80612 Immunogen Aac80617 Immunogen CpG oligo CpG oligo Immunosti Immunosti Imminorea Immunosti Immunosti Immunosti Immunosti Immunosti Immunosti Immunost Aas09588
Ab13558
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Acc48295 SUMMARIES AAS09588 ABL35568 ABL35579 AAC80612 AAC80617 AAC80623 AAC80623 AAS09622 AAS09582 AAS09582 AAS09583 AAS09583 AAC80652 AAC80614 ABK46466 ACC48309 ACC48295 ABK46500 ABK46460 ABK46465 ABL35612 ABK46462 80 Length % Query Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 00 Score Result

Acc48310 CpG oligo Acc48316 CpG oligo Acc83150 D class O	2446 2000 2000	Add51789 D19 SEQ I Add01074 CpG p oli Add01048 CpG D oli Abl35574 Immunosti Abl35618 Immunosti	Abl35601 Immunosti Abl35589 Immunosti Abl35607 Immunosti Abl35600 Immunosti Abl35607 Immunosti	3237 II
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## ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_29Jan04:\*

Database

genesegn1980s:\*

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; aschma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiaschmatic; dermatological; phosphorothioate; ss. Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:72. 12-APR-2000; 2000WO-US009839 12-APR-1999; 99US-0128898P AAC80652 standard, DNA; 20 (first entry) WO200061151-A2 14-FEB-2001 19-0CT-2000 Synthetic. AAC80652, AAC80652 

ä Verthelyi Klinman D, Ishii K, (KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERI/) VERTHELYI D.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

WPI; 2001-006880/01.

Claim 4; Page 35; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides

us-10-068-160-1.rng

CC (AACBOSB1-CB0723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NMN-Top-WanNA-9'-Do-WanN \$

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Gaps . 0 'Match 100.0%; Score 20; DB 4; Length 20; Local Similarity 100.0%; Pred. No. 3; es 20; Conservative 0; Mismatches 0; Indels Query Match Best Loca Matches

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ò d RESULT 2

AAC80614 standard; DNA; 20 BP.

AAC80614;

14-FBB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:34.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; asthma; infection; bacterial; viral; fungal; protozoal; parastic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; antimune deficiency; bloopgical warfare agent; cytostatic; antiarthritic; antimatorobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. 

WO200061151-A2

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The invention relates to novel immunogenic CpG oligodeoxynuclectides (AAC8081-881033). The oligonuclectide are at least 10 bases long and comprise one of the generic sequences 5.NNNT-CpG-WNNN-3. or 5.RY-CpG-RY comprise one of the generic sequences 5.NNNT-CpG-WNNN-3. or 5.RY-CpG-RY comprise one of the generic sequences 5.NNNT-CpG-WNNN-3. or 5.RY-CpG-RY complex comprising an oligonuclectide of the invention and a targetting a appart, and a pharmaceutical composition comprising the oligonuclectide of the invention and a targetting a equat. The oligonuclectide of the sequence 5.NNT-CpG-WNNN-3. Collator complex complex and those of the sequence 5.NNT-CpG-WNNN-3. The oligonuclectide of the sequence 5.NNT-CpG-WNNN-3. Collator collator of the sequence 5.NNT-CpG-WNN-3. Collator collator of the sequence 5.NNT-CpG-WNN-3. Collator collator collator of the sequence 5.NNT-CpG-WNN-3. Collator collator
                                                                                                                                                                                                                                                                                                                                Novel oligonuclectides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.
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                                                                                                                                                                                                                                         Verthelyi D;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 29; 46pp; English.
                                              12-APR-2000; 2000WO-US009839.
                                                                                            99US-0128898P.
                                                                                                                                                                                                                                      Klinman D, Ishii K,
                                                                                                                                                                 (ISHI/) ISHII K.
(VERT/) VERTHELYI D.
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                                                                                                                                          (KLIN/) KLINMAN D.
                                                                                            12-APR-1999;
19-OCT-2000.
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Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Gaps ó ch 100.0%; Score 20; DB 4; Length 20; Similarity 100.0%; Pred. No. 3; 20; Conservative 0; Mismatches 0; Indels Query Match Best Local ( datches

GGTGCATCGATGCAGGGGG 20 GCTGCATCGATGCAGGGGGG 20

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AAC80612 standard; DNA; 20

RESULT 3
AAC80612
ID AAC80

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AAC80612;

(first entry) 14-FEB-2001

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:32,

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; MK cell activation; cell-mediated immune response; 1-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; altergy, astehma, infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AlDS; autoimmune disease; lugus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; bloogical warfare agent; cytostatic; antiarthritic; antiathmatic; dermatological; phosphorothioate; se.

Synthetic.

WO200061151-A2.

19-OCT-2000.

12-APR-2000; 2000WO-US009839.

99US-0128898P 12-APR-1999;

KLIN/) KLINMAN D.

ISHII (/IHSI

VERT/) VERTHELYI D.

Verthelyi Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 29; 46pp; English.

ö immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention ö 100.0%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 3; 0; Indels Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other; 0; Mismatches 1 GGTGCATCGATGCAGGGGG 20 1 Gergearceargeagge 20 20; Conservative Local Similarity Query Match Best Loc Matches 8888888 ઠે g

AAC80617 RESULT

AAC80617 standard; DNA; 20 BP 

AAC80617;

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:37.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; ortokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; B-cell response; antibody production; immune response induction; vaccine; parassitic; tuberculosis; AlDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; ortostatic; antiarthritic; antiathmatic; dermatological; phosphorothioate; ss.

Synthetic.

WO200061151-A2.

19-OCT-2000.

12-APR-2000; 2000WO-US009839

99US-0128898P. 12-APR-1999;

(KLIN/) KLINMAN D.

(ISHI/) ISHII K. (VBRI/) VERTHELYI D.

Ishii K, Klinman D,

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**Verthelyi** 

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 29; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5.-NNT-CpG-WNN-3' or 5'-RY-CpG-RY -3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targetting agent, and a pharmaceutical composition comprising the oligonucleotide agent, and a pharmaceutical lomposition comprising the oligonucleotide mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a

cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
being able to induce a humoral response. It is thought that after
administration, the oligomucleotide acts on antigen-presenting cells
(e.g., macrophages and dendritic cells), which then release cytokines,
leading to activation of natural killer (NK) cells. A cell-mediated or
humoral response can then occur by activation of T- or B-cells. The
induction of an immune response is useful for treating, preventing or
ameliorating an allergic reaction (preferably aschma), or an infection,
where an immunogenic CpG oligomucleotide is administered either alone or
it combination with an anti-allergenic agent or anti-infectious agent.
The allergic conditions which may be treated include eczema, allergic
rhinitis, hayfever, urticaria, food allergies and other atopic
conditions, and the infections which may be treated include viral,
bacterial, fungal and protozoal infections such as tuberculosis AIDS,
bacterial, fungal and protozoal infections such as tuberculosis AIDS,
conditions, and the infections which may be treated include viral,
bacterial, fungal and spotozoal infections such as tuberculosis AIDS,
conditions, and the infections with an auti-input sclerosis,
conditions, and the infections with an auti-cancer
associated with immune system deficiency, and symptoms resulting from
exposure to an agent of bloggical warfare. An immunogenic CpG
oligonucleotide, either alone or in combination with an anti-cancer
agent, is useful for treating solid tumour cancer. The induction of an
immune response is used in antisense therapy and to improve the efficacy
continued to an expense of the preferably administered to
the immune and antisers preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention 

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

0; Gaps 100.0%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 3; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 20, Conservative

ò g RESULT 5 AAC80618

AAC80618 standard; DNA; 20 BP

AAC80618;

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynuclectide, SEQ ID NO:38.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell.-mediated immune response; humoral response; humoral response; B-cell response; humoral response; antibody production; immune response induction; vaccine; allergy; astchma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; se.

WO200061151-A2.

19-0CT-2000

12-APR-2000; 2000WO-US009839.

99US-0128898P. 12-APR-1999;

(KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERI/) VERTHELYI D.

```
The invention relates to novel immunogenic CpG oligodeoxymucleotides (AAC80581-C80723). The oligomucleotide are at least 10 bases long and comprise one of the generic sequences? *\text{NNN-205-WNNN-3} or 5.\text{RY-CpG-RY-C3}. The central CpG motif is unmerthylated, and the oligomucleotides or comprise one of the generic sequences $\text{NNN-105-WNNN-3} or 5.\text{RY-CpG-RY-C3}. The central CpG motif is unmerthylated, and chosen them more resistant to degradation. The invention also relates to an oligomucleotide delivery complex compressing an oligomucleotide of the invention and a targetting again, and a pharmacentical composition comprising the oligomucleotide delivery complex. The oligomucleotides are able to induce a cell-mediated response or a humoral (B-cell, antibody) response, with oligomucleotides and those of the sequence 5'-RY-CpG-RY-3' being able to induce a humoral response. It is thought that after cell-mediated response, and those of the sequence 5'-RY-CpG-RYNN-3' being able to induce a humoral response. It is thought that after cadministration, the oligomucleotide acts on antigen-presenting colls of leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T or B-cells. The induction of an immune response is useful for treating, preventing or amelioration which an anti-allergenic agent or antigeneric atopic of the combination which may be treated include eczema allergic conditions which may be treated include viral, beacterial, fungal and protozoal infections such a treated include eczema allergic conditions with manne assons induction may also be expensed in the treatment of an autoimmune disorder (e.g., lugus conditions of an agent of biological warfare, all
                                                                                                         Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numnne response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Verthelyi D;
                                                                                                                                                                                                                            Claim 4; Page 30; 46pp; English.
   Ishii K,
                                                         WPI; 2001-006880/01.
   Klinman D,
```

ö 100.0%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 3; 0; Indels tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 20; Conservative Query Match

GITCCATCGATCCAGGGGGG 20 1 GGTGCATCGATGCAGGGGG 20

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AACB0623 standard; DNA; 20 BP RESULT 6 AAC80623

AAC80623;

(first entry) 14-FEB-2001 Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:43.

CpG oligodecxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytckine release; natural killer cell; MK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response induction; vaccine; 0X2X6X8X8X8

L()

allergy, asthma, infection; bacterial, viral; fungal, protozoal, parasitic; tuberculosis, AIDS; autoimmune disease; lupus erythematosus, rheumatoid arthritis; multiple sclerosis; solid tumour; cancer, immune deficiency; biological warfare agent, cytostatic; antiarthritic; antimicrobial; antiallergic, protozoacide, tuberculostatic, antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. 

Synthetic

WO200061151-A2.

19-0CT-2000.

12-APR-2000; 2000WO-US009839.

99US-0128898P. 12-APR-1999;

(VERT/) VERTHBLYI D. (KLIN/) KLINMAN D.

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonuclectides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English

The invention relates to novel immunogenic CpG oligodeoxymucleotides CAAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5.\*NNTM-CpG-MNN-3' or 5.\*RX-CpG-RXY -3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide delivery complex the oligonucleotide of the invention and a targetting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotide are able to induce either a cell-mediated response or a humoral [B-cell, antibody) response, with coligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-RNT-CpG-WNNW-3' coligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a humoral response. It is thought that after a cell-mediated response, and dendritic cells), which then release cytokines, leading the oritivation of natural killer (NK) cells. A cell-mediated or numbination of natural killer (NK) cells. A cell-mediated or numbination with an anti-allergence and an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or antifections agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include eczema, allergic rised may into may also be constitions, and the infections which may be treated include viral, beacterial, fungal and protozoal infections such a tuberculosis, and secure of a securing an adsorber of a securing and multiple sclerosis, a disease associated with immune system deficiency, and symptoms resulting from exponence to an agent of biological warfare. An immunogenic of pidonucleoride situation with an anti-former of pidonucleoride setue he response is used in antisense therapy and to improve the efficacy vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention oligonuclectide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an

BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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DB 4; Length 20;
Score 20;
Pred. No.
100.0%;
Query Match
Best Local Similarity
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conclections comprising multiple Cog sequences, where one of the Cpd sequences is different from another of the multiple CpG sequences. The couledctides comprising an immune response, preferably a cell-capture induction an immune response, preferably a cell-capture induction in the response, involving non-B cell activation, interference confidence, involving non-B cell activation, interference cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disease, a disease associated with the immune capture to bio-warfare agent in a human. The induction of immune response improves the efficiacy of a vaccine and is used in antisease therapy. The ODN are useful for treating, preventing or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficiacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus crythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Prancisella, schistosmissis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, symptoms resulting from exposure of bio-warfare agent, including Ebola, ö Symptoms CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; blo-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Prancisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss. AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 Gaps prevent an allergic reaction, cancer, an autoimmune disorder and sym; resulting from exposure to bio-warfare agents, comprise multiple CpG Oligodeoxynucleotides for inducing an immune response to treat and ; Immunoreactive CpG sequence-containing oligonucleotide #72. Indels ö Mismatches (USSH ) US DEPT HEALTH & HUMAN SERVICES. Verthelyi D; 20 Gerecercearceaedede ö Claim 5; Page 39; 48pp; English. 1 GGTGCATCGATGCAGGGGG В 12-JAN-2001; 2001WO-US001122. 14-JAN-2000; 2000US-0176115P. AAS09622 standard; DNA; 20 (first entry) 20; Conservative Ishii K, Anthrax and Listeria WPI; 2001-442129/47. WO200151500-A1. 26-SEP-2001 19-JUL-2001 Klinman D, Synthetic. AAS09622; sednences Matches RESULT 7 à 윰

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other; ch 1 Similarity 100.0%; P 20; Conservative 0; 1 GGTGCATCGATGCAGGGGGG Query Match Local Matches X 8 ò 쉱

1 GGTGCATCGATGCAGGGGG 20 RESULT 8 AAS09582

AAS09582 standard; DNA; 20 BP AAS09582:

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #32.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; autisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001

12-JAN-2001; 2001WO-US001122

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D;

Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences

Claim 5; Page 32; 48pp; English.

induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus infection AASO9551-AASO9662 represent oligodeoxymucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, preferably a cell-mediated immune response involving non-B cell activation, interferon gamma (IRN-gamma) production on a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumnur cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection, a symptom resulting from exposure to bio-warfare agent in a human. The 

erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria 88888888

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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Gaps

.. O

0; Indels

Mismatches

50

Score 20; DB 4; Length 20; Pred. No. 3;

Gaps ö DB 4; Length 20; 0; Indels Mismatches ω •• Score 20; Pred. No. ö 100.0%; 20; Conservative 0 Best Local Similarity Query Match Matches

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ઠે 셤 AAS09587

ВЪ. AAS09587 standard; DNA; 20

AAS09587;

(first entry) 26-SEP-2001

Immunoreactive CpG sequence-containing oligonucleotide #37.

IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; altergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; utticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lugus erythematosus; rheumatond arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmanla; Ebola; Anthrax; Listeria; ss. sequence; immune response; non-B cell activation; interferon gamma;

Synthetic.

WO200151500-A1

19-JUL-2001.

12-JAN-2001, 2001WO-US001122,

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D;

Ishii K,

Klinman D,

WPI; 2001-442129/47.

Oligodeoxynuclectides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences 

Claim 5; Page 33; 48pp; English.

nucleotides comprising multiple CDG sequences, where one of the CDG sequences is different from another of the multiple CDG sequences. The ODM are useful for inducing an immune response, preferably a cell-mediated immune response, preferably a cell-interferon gamma (IFN-gamma) production or a humoral immune response involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliocating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least

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ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Prancisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola,
                                                                                                                                                                                                                                                                         Anthrax and Listeria
   888888888888888888
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Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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Score 20; DB 4; Length 20;
Pred. No. 3;
                           0; Indels
                           Mismatches
                                                             1 GGTGCATCGATGCAGGGGG 20
                           .
Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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AAS09593 standard; DNA; 20 AAS09593; AAS09593 

26-SEP-2001

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Immunoreactive CpG sequence-containing oligonucleotide #43. (first entry)

CpG sequence, immune response, non-B cell activation; interferon gamma; theragamma; humoral; antibody production; interleukin-6 production; therapoutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2002WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG seguences

Claim 5; Page 34; 48pp; English.

AASO9551-AASO9662 represent oligodeoxymuclectides (ODN) of at least 10 nuclectides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, professions interferon gamma (IRN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma,

system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic thinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthitis and multiple sclerosis, infections including Franciscials, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishhania and symptoms resulting from exposure of bio-warfare agent, including Ebola, with the immune Anthrax and Listeria

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Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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Gaps ..

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Gape
                            ö
  4; Length 20;
                          0; Indels
100.0%; Score 20; DB
100.0%; Pred. No. 3;
ive 0; Mismatches
                                                   1 GCTGCATCGATGCAGGGGG 20
                                                                         20
                                                                1 GGTGCATCGATGCAGGGGG
             Best Local Similarity 100.
Matches 20; Conservative
  Query Match
                                                   ò
                                                                        g
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RESULT 11 AAS09584

AAS09584 standard; DNA; 20

AAS09584;

(first entry) 26-SEP-2001 Immunoreactive CpG sequence-containing oligonucleotide #34.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autosimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lugus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmanla; Ebola, Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences.

Claim 5; Page 32; 48pp; English.

9 AASO9551-AASO9662 represent oligodeoxymucleotides (ODM) of at least nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. T 

Claim 5; Page 33; 48pp; English.

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con mediated immune response, preferably a cell-
mediated immune response, involving non-B cell activation, interferon
cell activation, antibody and interleukin-6 production in a host, for
treating, preventing or ameliorating an allergic reaction, e.g. asthma,
cancer, e.g. solid tumour cancer, a disease associated with the immune
cystem e.g. autoimmune disorder or an immune system deficiency, infection
or a symptom resulting from exposure to bio-warfare agent in a human. The
induction of immune response improves the efficacy of a vaccine and is
used in antisense therapy. The ONN are useful for treating, preventing or
ameliorating allergic reactions, including eccema, allergic thinits or
coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
and other atopic conditions, for improving the efficacy of vaccines
and other atopic conditions, for improving the efficacy of vaccines
and alaria, for treating immune system deficiencies, e.g. lupus
erythematosus and autoimmune diseases such as rheumatoid arthritis and
aularia, for treating immune system deficiencies, e.g. lupus
cultiple sclerosis, infections infections fincluding Francisella, schistosmiaais,
tuberculosis, acquired immunodeficiency symptome (AlDS), Leishmania and
symptoms resulting from exposure of bio-warfare agent, including Ebola,
              88888888888888888888888888
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Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

ö 100.0%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 3; 0; Indels Mismatches 0, Local Similarity 100. les 20; Conservative Query Match Matches

ö

1 GGTGCATCGATGCAGGGGGG 20 20 GGTGCATCGATGCAGGGGGG

ò 음 RESULT 12

BP AAS09588 standard; DNA; 20

AAS09588;

(first entry)

26-SEP-2001

Immunoreactive CpG sequence-containing oligonucleotide #38.

CDG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; IFN-gamma; buncer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; hupus erythematosus; theumatoid arthritis; multiple sclerosis; schistcosmisais; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001

14-JAN-2000; 2000US-0176115P.

12-JAN-2001; 2001WO-US001122.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG secuences

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nucleotides comprising multiple Cos sequences, where one of the cost sequences is different from another of the multiple Cos sequences. The ODM are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon garma (IFN-gamma) production or a humoral immune response involving B cell activation, interferon garma (IFN-gamma) production or a humoral immune response involving B cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disease, a system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or and other atopic conditions, including eczema, allergic relactions, including eczema, allergic reactions, including eczema, allergic relactions or coryza, hay fever, bronchial asthma, unticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiencies, e.g. lupus malaria, for treating immune system deficiencies, e.g. lupus and allergies and elemented in the proformation in the proposition of the strong and activation in the proformation are settle deficiencies, e.g. lupus and allergies and contraction are succined as rheumatogia entraction are settle deficiencies, e.g. lupus and allergies and contraction are succined as rheumatogia entraction are succined as rheumatogia entractions and autoin malaria, for treating immune system deficiencies, e.g. lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola,
                                                              represent oligodeoxynucleotides (ODN) of at least 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple sclerosis, infections including Francisella, schistosomiasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 4; Length 20;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthrax and Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                              AAS09551-AAS09662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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20 1 gerecarcearecageses 8 ABL35568 standard; DNA; 20 RESULT 13 ABL35568 ద

1 GGTGCATCCATGCAGGGGG 20

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(first entry) 04-APR-2002 ABL35568;

Immunostimulatory oligonucleotide SEQ ID NO: 494.

infection; allergy; cancer; hypersensitivity; bio-warfare; immunostiuulant; antialergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss. DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

Synthetic.

Location/Qualifiers 1. .20 /\*tag= Key misc\_RNA

/note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

WO200193902-A2

13-DEC-2001.

07-JUN-2001; 2001WO-US018276.

07-JUN-2000; 2000US-0209797P.

(BIOS-) BIOSYNEXUS INC. 

Flora M, Klinman DM; Mond JJ,

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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be useful for enhancing an immune response treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                 New immunostimulatory compositions comprising RNA/DNA hybrid obligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA/RNA bybrid; phosphorothicate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bic-warfare; immunostimulant, antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= Toptionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar*
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory oligonucleotide SEQ ID NO: 505.
                                                                                                                                     Example 11; Page 61; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGTGCATCGATGCAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
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hes 20; Conservative
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              WPI; 2002-130570/17.
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                                                                                                                                                                                                                                                                                                                                                                                the invention
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misc_RNA
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytckines. It can be useful for enhancing an immune response or inducing cytckines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant treating diseases, including pathogenic infection, (non-)malignant colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                              oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacerial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "optionally thymidine is replaced by uracil to
form RNA or DKA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
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                   compositions comprising RNA/DNA hybrid
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                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory oligonucleotide SEQ ID NO: 538.
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB
100.0%; Pred. No. 3;
ive 0; Mismatches
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                                                                                                       Example 11; Page 61; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCATCGATGCAGGGGG
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               New immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-130570/17.
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                                                                                                                                                                                                                                                                                                                                                          the invention
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Gaps ö

Indels

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Migmatches

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Score 20; DB 6; Length 20; Pred. No. 3;

oligonucleotides, useful for enhancing an immune response or inducing cytokinnes, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

Example 11; Page 61; 68pp; English.

The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant treating diseases, including pathogenic infection, (non-)malignant colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention 

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Gaps ô Cuery Match 100.0%; Score 20; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 3; Matches 20; Conservative 0; Mismatches 0; Indels

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1 GGTGCATCGATGCAGGGGG 20

ð g

1 GGTGCATCGATGCAGGGGG 20

Search completed: July 2, 2004, 08:31:32 Job time : 151.878 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 2, 2004, 08:09:30 ; Search time 31.3415 Seconds (without alignments) 354.132 Million cell updates/sec Run on:

US-10-068-160-1 20

Title: Perfect score: Sequence:

1 ggtgcatcgatgcagggggg 20

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched:

Total number of hits satisfying chosen parameters:

1365418

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\* Database :

/cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/GOMB.seq:\*
/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

		æ			SOFTERS	
Result		Query	:	!	;	-
	SCORE	Match	Length	g :	ID	Description
н		79.0	3358	m	US-09-248-571-2	Sequence 2, Appli
7	•	79.0	3358	v	-553-7	7
0	15.2	76.0	1584	**	US-09-252-991A-7138	713
Ω	•	76.0	1794	4	US-09-252-991A-7259	7255
ß	•	76.0	1872	ぜ	US-09-252-991A-7359	7359
φ		74.0	622	m	US-09-129-030-46	46,
	14.4	72.0	759	4	19-25	
ω υ	4.	72.0	1086	₹	US-09-252-991A-13644	1364
ψ φ	14.4	72.0	1092	4	39-25	1344
10		72.0	1194	4	US-09-252-991A-13697	136
11	14.4	72.0	1308	び	US-09-252-991A-1592	15
c 12	14.4	72.0	1356	4	39-25	14
13	14.4	72.0	3591	4	US-09-252-991A-1690	16
П	14.4	72.0	4280	4	US-09-079-592-1	H
c 15	74.4	72.0	5496	4	US-09-462-284-1	٦,
7	14.4	72.0	32654	4	US-09-801-191A-3	'n
7	14.4	72.0	1664976		US-08-916-421B-1	Н
18	14.4	72.0	4403765	(L)	US-09-103-840A-2	Sequence 2, Appli
19	4.	72.0	4411529		US-09-103-840A-1	Н
0		71.0	236	4,	19-621-	18
c 21	14.2	71.0	339	4	US-09-107-532A-3414	341
22	•	71.0	583	-	-08-454-	3, Appl
	٠	71.0	583	ო	US-09-064-033-3	m
24	4	71.0	583	4	-09-291-	m
25	14.2		1020	4	-03	1250,
26	•	71.0	1029	~	637B-19	191,
27	14.2	71.0	1128	4	US-09-107-532A-210	N

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 219, Appli Sequence 95, Appli Sequence 96, Appli	Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
US-08-454-196-1 US-09-064-033-1 US-09-291-046-1 US-09-328-857A-1 US-09-328-857A-1 US-08-615-170-4 US-09-312-283C-213 US-09-312-283C-213 US-09-312-283C-213 US-09-312-283C-213 US-09-023-655-991 US-09-598-401C-96 US-09-598-401C-96 US-09-598-401C-96 US-09-598-401C-96 US-09-598-401C-96 US-09-598-401C-96	US-08-456-837-6 US-08-457-342-6 US-08-457-646A-6
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11140 11140 11140 11392 11666	28958 28958 28958
71.0 71.0 71.0 71.0 71.0 71.0 71.0 71.0	999
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	14.2 14.2 14.2
2266666666666444 8904264967890112	4 4 4 4 4 5
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## ALIGNMENTS

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Sequence 2, Application US/09248571
; Batent No. 6136539
; GABREAL INFORMATION:
APPLICANT: BASBAUW, CAROL
APPLICANT: GALLUP, WARIANNE
APPLICANT: GENSCH, ERIN
TITLE OF INVERTION:
TITLE OF INVERTION: GENE EXPRESSION
TITLE OF INVERTION: GENE EXPRESSION
TITLE OF INVERTION: GENE EXPRESSION
TITLE OF INVERTION: CONFOSTIONS AND METHODS FOR INHIBITION OF MUCIN
TITLE OF INVERTION: GENE EXPRESSION
TITLE OF INVERTION UNMERR: 06/074,398
SARLIER PILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
TENCIN AND ACCOUNTS AND METHODS OF SECOND OF SECO
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-248-571-2
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.. o 79.0%; Score 15.8; DB 3; Length 3358; 89.5%; Pred. No. 71; 20.00; Mismatches 2; Indels 0 2 GIGCATCGAIGCAGGGGG 20 Query Match
Best Local Similarity 89.5
Matches 17; Conservative ò

998 drecaccardcaddedg 1016

g

US-09-553-736-2

| Sequence 2, Application US/09553736
| Patent No. 6440672
| Patent No. 6440670:
| APPLICANT: BASBAUM, Carol
| APPLICANT: GALUP, Marianne
| APPLICANT: GALUP, Marianne
| APPLICANT: GERRENICHAEL, Assefa
| APPLICANT: GERRENICHAEL, Assefa
| APPLICANT: GERRENICHAEL, ASSEFA
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
| TITLE OF INVENTION: MUCIN GENE EXPRESSION
| TITLE OF INVENTION: MUCIN GENE EXPRESSION
| TITLE OF INVENTION: MUSER: US/09/553,736
| CURRENT APPLICATION NUMBER: US/09/553,736
| PRIOR APPLICATION NUMBER: US 09/248,571

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GENERAL INFORMATION:
APPLICANT: MAC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7359
LENGTH: 1872
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Sequence 46, Application US/09129030A

Patent No. 624221

GENERAL INFORMATION:
FOLKE MATION:
FILE PERFERENCE: 5070-2071-005

FILE REPRENCE: 5070-2071-005

CURRENT APPLICATION NUMBER: US/09/129,030A

CURRENT PILING DATE: 1998-08-04

EARLIER APPLICATION NUMBER: AU PN7856

EARLIER PILING DATE: 1996-02-05

EARLIER PILING DATE: 1996-02-05

EARLIER PILING DATE: 1996-02-16

EARLIER PILING DATE: 1996-02-16

EARLIER PILING DATE: 1996-02-16

EARLIER PILING DATE: 1997-01-24

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 46

LENGTH: 622
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0
           76.0%; Score 15.2; DB 4; Length 1794; llarity 85.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.0%; Score 15.2; DB 4; Length 1872; Best Local Similarity 85.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 622;
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Pred. No. 1.9e+02;
0; Mismatches 2;
                                                                                                                                                                  208 GCCCCAGCGATGCAGGGTGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 GGCGCAGCGATGCAGGGTGG 290
                                                                                                               1 GGTGCATCGATGCAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7359
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88.9%;
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Best Local Similarity 88.5
Matches 16; Conservative
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US-09-129-030-46
                                 Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                         US-09-252-991A-7359
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NAME/KEY: CDS
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NAME/KEY: CDS
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           Query Match
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US-09-252-991A-7138/C
i Sequence 7134, Application US/09252991A
i Sequence 7134, Application US/09252991A
i Sequence 7135, Application US/09252991A
i Patent No. 6551795
i GENERAL INFORMATION:
I TILLE OF INVENTION: NUCLEIC ACID AND AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS
I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PLING DATE: 1999-02-18
I PRIOR PLILOM NUMBER: US 60/074,788
I PRIOR PLILOM NUMBER: US 60/074,788
I PRIOR PLILOM NUMBER: US 60/074,190
I PRIOR PLILOM NUMBER: US 60/094,190
I PRIOR FILING DATE: 1998-07-27
I NUMBER OF SEQ ID NOS: 33142
I LENGTH: 1584
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Sequence 7259, Application US/09252991A

Patent No. 651795

GENERAL INPORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1794
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                                                                                                                                                                                                                                                                                             Score 15.8; DB 4; Length 3358;
Pred. No. 71;
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                                                                                                                                                                                                                                                                                          Ouery Match 79.0%; Score 15.8; Dest Local Similarity 89.5%; Pred. No. 71; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                 60/074,398
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7259
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PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US ¢
PRIOR FILING DATE: 1998-02-11
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                           NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver.
SEQ ID NO 2
LENGTH: 3358
                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
US-09-553-736-2
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ACIDICAL CALD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT PELLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13444
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Patent No. 6551752
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/06/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Sequence 13697, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION: BUCHEL AL

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING 7

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PLLICATION NUMBER: US 60/074,788

PRIOR PLLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13697

LENGTH: 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72.0%; Score 14.4; DB 4;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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| Sequence 13644, Application US/09252991A
| Sequence 13644, Application US/09252991A
| Sequence 13644, Application US/09252991A
| Application No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US 60/074,788
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-02-27
| NUMBER OF SEQ ID NOS: 33142
| ERNOTH: 1086
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196_136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

FRIOR FILING DATE: 1998-07-27

FRIOR FILING DATE: 1998-07-27

FRIOR FILING DATE: 1998-07-27

SEQ ID NOS: 33142

ENGTH: 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Pest Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1;
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; Sequence 1486, Application US/09252991A
; Patent No. 6551795
                                                                          217 Grácarcaarácaacaca 234
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ORGANISM: Pseudomonas aeruginosa
                          2 GTGCATCGATGCAGGGG 19
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APPLICANT: Kimberly Brown
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Alan Klotz
APPLICANT: Tony Byun
TITLE OF INVENTION: Polypeptides Having Dipeptidyl
TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
FILE REPERENCE: 5524.200-00.
CURRENT APPLICATION NUMBER: US/09/079,592B
CURRENT FILING DATE: 1998-05-15
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Pred. No. 3.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08857,884
PRIOR FILING DATE: 1997-05-16
PRIOR FILING DATE: 1997-05-16
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
EAG ID NO 1
LENGTH: 4280
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US-09-462-284-1/C
| Sequence 1, Application US/09462284 |
| Patent No. 6309868 |
| GENERAL INVENMATION: |
| APPLICANT: Nestec S.A. |
| APPLICANT: Monod, Michel |
| APPLICANT: Monod, Michel |
| APPLICANT: Affolter, Michel |
| APPLICANT: Van Den Broek, Peter |
| TITLE OF INVENTION: CLONING OF THE |
| TITLE OF INVENTION: ROLYL-DIEBPTIDYL-PBEP; FILLE REFRESHUES: 8265-298 |
| CIRPERUM: NOWELLOWER |
| CIRPERUM: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                         Sequence 1, Application US/09079592B
Patent No. 6664092
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                                                                                                                                                                                                                                                                                                                 Alexander Blinkovsky
293 GGTGCGTCGATGCAGG 308
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Best Local Similarity 93.8
Matches 15, Conservative
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CORGANISM: Aspergillus
US-09-079-592-1
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SOPTWARE: FastSEQ for
SEQ ID NO 1
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APPLICANT: Alexand
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ORGANISM: Fungus
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Sequence 1425, Application US/09252991A
Sequence 1425, Application US/09252991A
Sequence 1425, Application US/09252991A
Patent No. 6511795
GENERAL INPORMATION:
APPLICANT:
Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 101196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1425
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1690
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                                                                                                                                                                                                     Query Match
72.0%; Score 14.4; DB 4; Length 1308;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                             ; LENGTH: 1308
; TYPE: DNA,
; ORGANISM: Peeudomonas aeruginosa
US-09-252-991A-1592
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1690
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SEQ ID NO 1592
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1 GGTGCATCGATGCAGG 16

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Search completed: July 2, 2004, 13:37:17 Job time: 38.3415 secs

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1 GGTGCATCGATGCAGGGGG 20
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Best Local Similarity 100.0
Matches 20; Conservative
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Sequence 505, App
Sequence 51, Appl
Sequence 14, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 38, Appl
Sequence 43, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 176, Appl
Sequence 500, Appl
                                                                    2, 2004, 08:11:05; Search time 154.146 Seconds (without alignments) 625.926 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/ cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/ cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US00_NEW_PUBCOMB.seq:*
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                                                                                                                                                                                                                 6326084
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-874-991C-505
US-00-874-991C-538
US-10-068-160-54
US-10-108-160-54
US-10-194-035-32
US-10-194-035-33
US-10-194-035-37
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US-10-194-035-38
US-10-194-035-37
US-10-194-035-43
US-10-194-035-43
US-10-194-035-43
US-10-194-035-176
US-10-194-035-176
US-10-666-022-177
US-10-666-022-177
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                                              OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1 ggtgcatcgatgcagggggg 20
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521, App
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US-09-874-991C-521
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US-09-874-991C-521
US-09-874-991C-521
US-09-874-991C-521
US-10-194-035-73
US-09-874-991C-499
US-09-874-991C-499
US-09-874-991C-510
US-10-68-160-11
US-110-68-160-11
US-110-68-160-37
US-110-68-160-37
US-110-68-160-35
US-110-68-160-55
US-110-194-035-81
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# AL I GNMENTS

Gaps Sequence 494, Application US/09874991C
| Publication No. US20040052763A1
| GENERAL INFORMATION:
| APPLICANT: MOND, JAMES J.
| APPLICANT: PLORA, MICHAEL
| APPLICANT: MOND, JAMES J.
| TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
| FILE REFERENCE: 07787.0042-0;
| CURRENT APPLICATION NUMBER: US/09/874,991C
| CURRENT FILING DATE: 2001-06-07
| PRIOR FILING DATE: 2000-06-07
| NUMBER OF SEQ ID NOS: 620
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 494 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-874-991C-494 ö 100.0%; Score 20; DB 13; Length 20; 100.0%; Pred. No. 3; Indels ö 0; Mismatches TYPE: DNA ORGANISM: Artificial Sequence

GTGCATCGATGCAGGGGG 20

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; Sequence 505, Application US/09874991C; Publication No. US20040052763A1

Gaps

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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: THE GOVERNMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: URTHHENTI, Danniela
FILIE OP INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILIE OP INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILIE REPRENCE: 4229-6199
CURRENT APPLICATION NUMBER: 60/128, 898
PRIOR PILING DATE: 1999-04-12
SPRIOR FILIEM DATE: 1999-04-12
SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: KSTHELY, Ken
APPLICANT: VERTHELY, Danniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REPRENENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
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Pred. No. 3;
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100.0%; Pred. No. 3;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
; FILE REPERENCE: 4239-61999; CURRENT APPLICATION NUMBER: US/10/068,160; CURRENT FILING DATE: 2002-02-06; PRIOR PEPLICATION NUMBER: 60/128,898; PRIOR PELING DATE: 1999-04-12; NUMBER OF SEQ ID NOS: 120; SOFTWARE: PatentIn version 3.1; ESMQ ID NO 1; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54, Application US/10068160 Publication No. US20030060440A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide US-10-068-160-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Oligonucleotide US-10-068-160-54
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Best Local Similarity 100.'
Matches 20; Conservative
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APPLICANT: KLINMAN, Dennis
APPLICANT: SHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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US-09-874-991C-538
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APPLICANT: MOND, JAMES J.
APPLICANT: MOND, JAMES J.
APPLICANT: MICHAEL
APPLICANT: KLINAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07087-0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
FRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID MOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 538
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                                                 APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPERRINCE: 07737, 0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 505
LENGTH: 20
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Publication No. US20030060440A1
GENERAL INFORMATION:
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                               : MOND, JAMES J.
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Matches 20; Conserv
  GENERAL INFORMATION:
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FULLIAGANT: USAUUJU144229A1

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE

APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: KLINMAN, Dennis

APPLICANT: USRTHELYI, Daniela

TILLA OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

FILLE REFERENCE: 4239-633.7

CURRENT APPLICATION NUMBER: US/10/194,035

CURRENT APPLICATION NUMBER: DO1-07-12

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 38

LENGTH: 20
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APPLICANT: KINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERTHELY!, Men
APPLICANT: VERTHELY!, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
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100.0%; Pred. No. 3;
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           CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 20
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Publication No. US20030144229A1
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ORGANISM: Artificial Sequence
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Matches 20; Conserv
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Publication No. US20030144229A1

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: ALIMARAN, Dennis
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: ALIMARAN, Dennis
APPLICANT: USHII, Ken
APPLICANT: USHII, Ken
APPLICANT: USHII, Ken
CURRENT FILING DATE: 2002-07-12
FILE REPRENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/101122
FRIOR APPLICATION NUMBER: US/10/101122
FRIOR APPLICATION NUMBER: US 60/176,115
FRIOR PELLING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 34
LENGTH: 20
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APPLICANT: THE COVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: THE COVERNMENT OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SSOFTWARE: Patentin Ver. 2.1
LENGTH: 20
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Matches 20, Conserv
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Screetary of the Department of Health and Human Services APPLICANT: Klinman, Dennis M. APPLICANT: Klinman, Dennis M. APPLICANT: Werthelyi, Daniela TITLE OF INVENTION: WETHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG FILE REPERRORE: 4239-66899 CURRENT FILLIAG DATE: 2003-09-17 PRIOR APPLICATION NUMBER: US/10/666,022 CURRENT FILLING DATE: 2003-09-17 PRIOR PILING DATE: 2003-09-17
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APPLICANT: FLORA, MICHAEL
APPLICANT: KLIMMAN, DENNIS M.
TITLE OF INVENTION: IMMOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07797-0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
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Pred. No.
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Pred. No.
                          CURRENT APPLICATION NUMBER: US/10/666,022 CURRENT FILING DATE: 2003-09-17
                                  PRIOR APPLICATION NUMBER: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SEQ ID NO 176
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p Sequence 177, Application US/10666022
publication No. US20040105872A1
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100. [
Matches 20; Conservative
       FILE REFERENCE: 4239-66899
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US-09-874-991C-500
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APPLICANT: Klinman, Dennis M.
APPLICANT: Varthelyi, Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: URTHELYI, Daniela
TITIE OF INVENTION: OLIGODECXNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TILE REPERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SCOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/10194035
Publication No. US20030144229A1
GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
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US-10-194-035-43
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CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR PILING DATE: 2000-01-14
NUMBER OF SZQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGTGCATCGATGCAGGGGG 20
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Best Local Similarity 100.0
Matches 20, Conservative
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US-10-666-022-176
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Query Match 100.0%; Score 20; DB 13; Length 22; Best Local Similarity 100.0%; Pred. No. 3; Matches 20; Conservative 0; Mismatches 0; Indels

1 GGTGCATCGATGCAGGGGG 20

8 8

Search completed: July 2, 2004, 13:58:23 Job time : 155.146 secs

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CG016914 PUIBLSTD
BXG39713 BXG39713
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CB055500 BST645181
BJ229325 BJ229325
CA920724 EST638442
BJ259509 BJ634520
BJ259701 BJ250701
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BJ753427 GSJ254442
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CA157948 SCEZRZ304
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CA157345 BGCSTC217
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BZ44980 BONDQ35TR
BH128747 G-3011 Ma
CC58288 GH20.386
AG073881 Pan trog1
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AL33377 Tetraodon
AL3331410 Tetraodon
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BQ860936 QGC17B11.
BZ063097 11G86b12.
BZ449138 BONHP21TF
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                                                                                                                                                                                                                                                                                                                                                    AV268287 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus CDNA clone 4930534F16 3', mRNA sequence.
                                   AV028453

AL622509

AL622509

BU229325

BU229325

CA920712

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AW325275

BB422123

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CB96650
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VERSION
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AV281636 AV281636
AV269637 AV269637
BI507147 BBI70025B
                                            2, 2004, 07:38:45; Search time 1497.8 Seconds (without alignments) 398.746 Million cell updates/sec
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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                               nucleic - nucleic search, using sw model
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Searched:

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S Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, Harayasu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Ich, M., Izawa, M., Kadora, K., Kagawa, I.,
Ishii, Y., Ishikawa, T., Kihuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
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Tsunoda, Y., Wataniki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokofa, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Konno, H., et al. 1999)
L. Onbett: Yoshihde Hayashizaki, M., Contect: Yoshihde Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome.resegec.riken.go.jp,
URLihttp://genome.gcc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 {7}, 3455-3460 {1998}
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 {5}, 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 {1999}
                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was cloned into the Xhol and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI."
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                     Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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(DH108F*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.rtc.riken.go.jp) for
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Best Local Similarity 94.7
Matches 18; Conservative
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AV281636 GI:6269673
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                        Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Okazaki,Y. acarminci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation System. Genome Res. 9 (5), 463-470 (1999)

Carminci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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(DH10B)
                                                                                                                                                                                                               Yoneda, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%; Score 18.4; DB 9; Length 257; larity 95.0%; Pred. No. 7.3e+02; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Mus musculus"
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                                                                                       Tel: 81-45-503-9222
Fax: 81-45-503-9216
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BACKWARD: ATTAACCTCACTAAAG
Plate: B170055820 row: H column: (
Seg primer: AGCGGATAACAATTTCACACAGGA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GTGCATCGAGGCAGGGGG 160
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Apis mellifera
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                                                                                                                                                                                                                                                                                                              Query Match
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PUBMED
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                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Buteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Buteleostomi;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Konno, H. Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Phkuda, S., Pukunishi, Y., Hara, A., Hayatsu, M., Hirozane, T., Hori, P., Kai, C., Kawai, J., Kikuchi, W., Kadota, K., Kagawa, I., Kai, C., Kawai, T., Miki, R., Mizuno, Y., Noya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Shibata, X., Suzuki, H., Salto, H., Sano, M., Sato, K., Shibata, Y., Suzuki, H., Takabashi, F., Tateno, M., Tominaga, N., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y. M. Umpublished (1999)
                                                                                                                                                                  AV269637 AVE69637 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930544G09 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 465-470 (1999) Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-res@qsc.riken.cn.in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-re@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., Matahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Tayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/67"
/db xref="taxon:1090"
/clone="4930544609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
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                                           GTGCATCGAGGCAGGGGG 102
20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .303
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VERSION
KEYWORDS
                                                                                                                    RESULT 3
AV269637
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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Email: generobledife.uluc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs Welloome Trust Innovation
Award in Functional Genomics to G.B. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
REPERT IN THE SEQUENCE
SIMPLE repeat STRAND (+) ELEMENT (A)n LOCATION [449,468].
                                                                                                                                                                                                               was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIS07147 11near EST 08-APR-2002 BB170025B20H07.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170025B20H07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 473)
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.B.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Apis mellifera"
/mol_type="mRNN"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Length 303;
                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 17.4; DB 9; Length 3
94.7%; Pred. No. 2.18+03;
cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
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GSS 13-JUL-1996

Buteleostomi;

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/note="Vector: sCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCACHRIO40C03.g HR1 Saccharum officinarum cDNA clone SCACHRIO40C03.g
S/, mRNA sequence.
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Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Harnes, G.A., Brond, T., Gillilan, B., Schagemann, C., Probst, S., Harris, J., Defoud, J., Wefarland, J., Burzinski, K., Khan, M., Kupfer, K. and Garner, H.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baccharum officinarum
Saccharum officinarum
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum
                                                                                                                         B01614 134910-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-134910, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="chimeric hamster somatic cell hybrid" /clone_lib="cSRL flow sorted Chromosome 11 specific cosmid"
                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bmail: gevans@utsw.swmed.edu, shanesmcdermott.swmed.edu
PCR PRimers
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85.0%; Score 17; DB 28; Length 54

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="cSRL-134910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 541.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: TACTAAAGCGAAGCTAGGTG BACKWARD: TTTGGACAGATTTAGCTCAG
       301 GGTGCACCGATGCAGGGGG 283
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                                                                                                                                                                                                                    B01614.1 GI:1410892
                                                                                                                                                                                                                                                                  Homo sapiens (human)
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Class: cosmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 214-648-1666
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                                                                                                                                                                                                                                                                                           Homo sapiens
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CA101677/c
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SOURCE
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B01614/c
LOCUS
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dissue_rype="melanotic melanoma, cell line"
/tissue_rype="melanotic melanoma, cell line"
/tissue_rype="melanotic melanoma, cell line"
/tissue_rype="melanotic melanoma; cell line"
/tissue_rype="melanotic por resistant)"
/db_host="nDHA MGC_112"
/clone_lib="nHH MGC_112"
/note="nOrgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="nOrgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="nOrgan: skin; Vector: poTB7; Site_1: Anote condition of complex made by oligo-dT priming. Directionally cloned into GGCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
Site 2: Not1: This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Scares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups.
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5', mRNA sequence.
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                                                                                                                                                                                                                                                                                           Length 473;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                      Score 17.4; DB 12;
Pred. No. 2.4e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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Best Local Simil
Matches 18; C
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KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT REFERENCE

FEATURES

ORIGIN

ACCESSION VERSION

RESULT 5 BQ898390/c LOCUS DEFINITION

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Class: sheared ends.
Location/Qualifiers
1. .839
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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BX639713
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Use Silva, da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCBST

The libraries that made SUCBST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda Molecular e Engenharia Genetica
Universidade Estadual de Campinas
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Bennetze, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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Unpublished (2003)
Other GSSs: PUIBJ87TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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http://www.rzpd.de/cgi.bin/products/showLib.pl.cgi/response?libNo=4 62 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
Fax: +20 30 32639 111
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 272)
Henrich,J., Hermanns,J., Kranz,H., Ioebbert,R., Schlueter,T.;
Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Mouse ArrayTAG cDNA (110N)
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
In Neu-heimeimer Feld 580, D-69120 Heidelberg, Germany
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/organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
/db.e="ZAMBTa0544P06"
/clone="ZAMBTa0544P06"
/clone="Za
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer:
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Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 0;
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Pred. No. 3.8e+03;
0; Mismatches 2;
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIOND462H0719"
/lab host="DH108"
/clone_lib="pBluescript Lion"
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mRNA linear EST 21-MAR-2002
cDNA clone NAH-P05-H-10-5, mRNA
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Contact: Christophides GK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="spike at flowering date"
/dev_stage="Feekes' scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
                                                                                                                                 Center For Genetic Resource Information
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National Institute of Genetics
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Email: tshini@genes nig.ac.jp.
Location/Qualifiers
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Buropean Molecular Biology Laboratory
Meyerhofstrasel, 69117 Heidelberg, Germany
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Plate: P05 row: H column: 10.
Location/Qualifiers
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84.0%; Score 16.8; DB 12;
Best Local Similarity 90.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
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                      1 (bases 1 to 631)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                               /mol type="mRNA"
/cultivar="Chinese Spring"
/db xref="taxon:4565"
/clone="whf16m07"
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/clone_lib="NAH"
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/db_xref="taxon:7165"
Pooldeae, Triticeae, Triticum
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AL692509.1 GI:19612418
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Buxaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Garninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahiza, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugame, M., Watanabe, S., Yagame, M., Yamamura, T., Nokot, T., Rikik Mouse ESTS

Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory

RIKEN
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Tel: 81-298-36-9145
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Fax: 81-298-36-91945
Fax: 81-298-36-91945
Fax: 81-298-36-91945
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 9512):520-524 (1998)
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                      AVO28453 Aus musculus adult C57BL/6J brain Mus musculus cDNA clone
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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BJ244833. GI:20057113
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/dev_stage="adult"
/clone_lib="Mus musculus adult C57Bi/6J brain"
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/strain="C57BL/63"
/db_xref="taxon:10090"
/clone="1432000G13"
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                                                                                                                               1432000G13, mRNA sequence.
                                                                                                                                                                                                                             Mus musculus (house mouse)
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Best Local Similarity 90.0
Matches 18; Conservative
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BJ229325 Y. Ogihara unpublished cDNA library, Wh_dL Friticum aestivum cDNA clone whdll9e17 3', mRNA sequence.
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EST638442 MTUS Medicago truncatula cDNA clone MTUS-31C10, mRNA
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Vandenbosch, K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)

Triticum aestivum (bread wheat)

Triticum aestivum

Triticum aestivum

Triticum aestivum

Bukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheop)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

I (bases I to 671)

S Ogihara, Y. and Mural, K.

Expressed genes in Triticum aestivum

Unpublished (2002)

Contact: Tadasu Shin-i

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Tel: 81-55-81-6855

Fax: 81-559-81-6855

Fax: 10-cation/Qualifiers
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/dev_stage="Feekes' scale 1"
/clone_lib="Y. Ogihara unpublished cDNA library,
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Unpublished (2002)
Contact: VandenBostor K
Contact: VandenBostor V
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90.0%; Pred. No. 4.9e+03;
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/cullivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whdl19e17"
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
KhoI; CDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda tap phage using Ex-assist
helper phage and propagated in SOLR cells."
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rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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/mol type="mrNA"
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/clone="HGA-10K1"
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TV plate 31 rotated 180 degrees at TIGR
TIGR sequence name: MTUBE63TV
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Seq primer: (gtA AtA CgA CTC ACT AtA ggg C).

Location/Qualifiers

1. 671

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Search completed: July 2, 2004, 13:32:50 Job time: 1502.92 secs

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Query Match 84.0%; Score 16.8; DB 14; Length 671; Best Local Similarity 90.0%; Pred. No. 4.9e+03; Matches 18; Conservative 0; Mismatches 2; Indels 0.

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July 2, 2004, 07:36:05; Search time 704.146 Seconds (without alignments) 1231.080 Million cell updates/sec
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GenCore version 5.1.6
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 507 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Patent: WO 0193902-A 514 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 496 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 504 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                 Mond, J.J., Flora, M. and Klinman, D.M.
Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 517 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 525 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 529 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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Sequence 525 from Patent WO0193902.
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Sequence 529 from Patent W00193902.
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AX352233.1 GI:18617516
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Vaccine against RSV
Vaccine against RSV
Batcht: WO 0211761-A 60 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 540 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers

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Sequence 517 from Patent WO0193902.
AX352221
               20 bp
Sequence 540 from Patent W00193902.
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Sequence 60 from Patent WO0211761.
AX465392 GI:21899755
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 101 19-UUL-2001;
Secretary of the Department of Health and Human Services (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 495 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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ative 0; Mismatches 1;
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Sequence 495 from Patent WO0193902.
AX352199.1 GI:18617482
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Sequence 101 from Patent WO0151500.
AX194501
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 548 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 537 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
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Sequence 537 from Patent W00193902.
AX352241 GI:18617524
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Sequence 548 from Patent WO0193902.
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Mond, J.J., Flora, M. and Klinman, D.M.
Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 499 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
1. 20
//organism="synthetic construct"
//mol\_type="unassigned DNA"
//db\_xref="taxon:32630"
//note="Synthetic HDR" AX352203 AX352203.1 GI:18617486 synthetic construct synthetic construct artificial sequences. ACCESSION VERSION KEYWORDS SOURCE ORGANISM source REFERENCE AUTHORS TITLE JOURNAL FEATURES

ORIGIN

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Query Match 92.0%; Score 18.4; DB 6; Length 20; Best Local Similarity 95.0%; Pred. No. 7.66+02; Matches 19; Conservative 0; Mismatches 1; Indels

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Search completed: July 2, 2004, 10:07:55 Job time: 705.146 secs

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July 2, 2004, 06:05:50; Search time 149.878 Seconds (without alignments) 566.887 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                               - nucleic search, using sw model
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Perfect score:
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1 ggtgcaccggtgcagggggg 20 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequi990s:\* genesequ2000s:\* genesequ2001as:\* genesequ2001bs:\* N Geneseq 29Jan04:\* : geneseqn1980s:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Aac80622 Immunogen	Aas09592 Immunorea	Abl35614 Immunosti	Abl35578 Immunosti	Abl35581 Immunosti	Abl35570 Immunosti	Abl35588 Immunosti	Abk46470 Immunosti	Acc48296 CpG oligo		Acc83118 D class C		Add01049 CpG D oli	Abl35599 Immunosti	Abl35603 Immunosti	Abl35591 Immunosti	Abl35611 Immunosti	Abl35622 Immunosti	Aas09651 Immunorea	Abl35573 Immunosti	Abl35584 Immunosti	Abl35569 Immunosti	Abl35617 Immunosti
ID	AAC80622	AAS09592	ABL35614	ABL35578	ABL35581	ABL35570	ABL35588	ABK46470	ACC48296	ACC48313	ACC83118	ACC83152	ADD01049	ABL35599	ABL35603	ABL35591	ABL35611	ABL35622	AAS09651	ABL35573	ABL35584	ABL35569	ABL35617
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	92.0	92.0	92.0	92.0	92.0
Score	20	20	20	20	20	20	20	20	20	20	20	20	20	9	20	20	20	20	18.4	18.4	18.4	18.4	18.4
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Abl35580 Immunosti Acc48311 CpG oligo Acc48320 CpG oligo Acc48321 CpG oligo	Acc83125 D class C Acc83116 D class C Acc83126 D class C Add01076 CpG D oli		онни	Aac80652 Immunogen Aac80722 Immunogen Aac80612 Immunogen Aac80612 Immunogen Aac80617 Immunogen
6 ABL35580 7 ACC48311 7 ACC48320 7 ACC48321	8 ACC83125 8 ACC83116 8 ACC83126 9 ADD01076		7 ACC48300 4 AAC80602 4 AAS09572 6 ABK46450	4 AAC80652 4 AAC80722 4 AAC80614 4 AAC80612 4 AAC80617
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4 2 2 2 4 2 6 2	30 30 31 31	0 W W W W	33 38 39 40	4 4 4 4 4 4 4 4 4 4 4 6 6 4 8

# ALIGNMENTS

RESULT 1

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42. ם AAC80622 standard; DNA; 20 (first entry) 14-FEB-2001 AAC80622; AAC80623 

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; immune response; particol, immune response; naticol, pacterial; immune response induction; vaccine; allery; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; immune deficiency; biological warfare agent; cytostatic; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimiatorobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss.

WO200061151-A2. 19-0CT-2000. Synthetic.

99US-0128898P. (ISHI/) ISHII K. (VERT/) VERTHELYI D. (KLIN/) KLINMAN D. 12-APR-1999;

12-APR-2000; 2000WO-US009839.

Verthelyi Ishii K, WPI; 2001-006880/01. Klinman D,

ä

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides

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Comprise one of the generic sequences 5.4NNY-CpG-WNNN-3 or 5.4XY-CpG-RY
comprise one of the generic sequences 5.4NNY-CpG-WNNN-3 or 5.4XY-CpG-RY
comprise one of the generic sequences 5.4NNY-CpG-WNNN-3 or 5.4XY-CpG-RY
complex comprising an oligonucleotide of the invention and a targetting
complex comprising an oligonucleotide of the invention and a targetting
complex comprising an oligonucleotide of the invention and a targetting
complex comprising an oligonucleotide of the invention and a targetting
complex complex. The oligonucleotide of the invention and a targetting
coligonucleotides of the sequence 5.4XY-CpG-RY-3
coligonucleotides a humoral response. It is thought that after
definistration, the oligonucleotide acts on antigon-presenting calls
coligonucleotide and dendriatic cells), which then release cytokines,
leading to activation of natural killer (MK) cells. A cell-mediated or
lunoral response can then occur by activation of T or B-cells. The
andiotration an allergic reaction (preferably asthma), or an infection,
where an immunogenic CpG oligonucleotide is administered either alone or
conditions, and the infections which may be treated include eczema, allergic
conditions, and the infections which may be treated include eczema,
conditions, and the infections which may be treated include eczema,
conditions, and the infections which may be treated include viral,
conditions, and the infections which may be treated include eczema,
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      The oligonucleotide are at least 10 bases long and
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; Score 20; DB 4; Length 20; Pred. No. 21; 0; Mismatches 0; Indels Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other; 1 GGTGCACCGGTGCAGGGGGG 20 1 Gerececerecaseses 20 100.0%; Query Match
Best Local Similarity 100.0%;
Watches 20; Conservative à

Gaps

AAS09592 standard; DNA; 20 BP. (first entry) 26-SEP-2001 AAS09592; RESULT 2 AAS09592 

Immunoreactive CpG sequence-containing oligonucleotide #42.

CpG sequence; immune response; non-B cell activation; interferon gamma; they gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; human immunodefictency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

WO200151500-A1

19-JUL-2001

12-JAN-2001; 2001WO-US001122

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Ishii K, Klinman D,

WPI; 2001-442129/47.

prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG response to treat and Oligodeoxynucleotides for inducing an immune sednences

Claim 5; Page 34; 48pp; English.

nucleotides comprising multiple CGS sequences, where one of the CGS sequences is different from another of the multiple CGS sequences. The comparison multiple CGS sequences, where one of the CGS sequences is different from another of the multiple CGS sequences. The CGS ob are useful for inducing an immune response, preferably a cell-cativation, interferon cancer in the conformal immune response involving B CG cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma. CC cancer, e.g. solid tumour cancer, a disease associated with the immune cystem deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is cused in antisense therapy. The CDN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, for improving the efficacy of vaccines can other atopic conditions, including Prancisella, schiztosomiasis, there were the control of the control (ODN) of at least 10 AAS09551-AAS09662 represent oligodecxynucleotides Anthrax and Listeria

Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

., Score 20; DB 4; Length 20; Pred. No. 21; Mismatches 0; Indel8 100.08; FIN 20; Conservative Query Match Best Local Similarity Matches

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ABL35614 standard; DNA; 20 BP 04-APR-2002 (first entry) ABL35614; RESULT 3 ABL35614 THE SOURCE SERVICES AND A SERVICES A

Immunostimulatory oligonucleotide SEQ ID NO: 540.

DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytoetatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; viruccide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

Synthetic.

Location/Qualifiers Key misc RNA

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                                                                                                                                                                                                                                                                                              The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant trumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
/*tag= a
/note="optionally thymidine is replaced by uracil to
/note="optionally thyprids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                             oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
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les 20; Conservative
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                                                        WO200193902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumnours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic thinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunosimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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least one other base through a ribose sugar"
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form RNA or DNA/RNA hybrids. Thymidine is li:
least one other base through a ribose sugar"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mond JJ, Flora M,
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytchines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, preventing or malaria. The composition is also useful for treating, preventing or maliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Boola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                         New immunostimulatory compositions comprising RNA/DNA hybrid oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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/notes "optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
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                                                                                                                                                                                                      Klinman DM;
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                                                                 07-JUN-2001; 2001WO-US018276.
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                                                                                                                                                           (BIOS-) BIOSYNEXUS INC.
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                    13-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              focus "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                    New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
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100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
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Score 20; DB 6; Length 20; Pred. No. 21; ; Mismatches 0; Indels

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                                                                                      Claim 4; Page 8; 30pp; English
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                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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   WPI; 2002-227118/28.
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Best Local Similarity
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modified_base
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Matches
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                                                                                                                                                        New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unmethylated CpG; oligdideoxynucleotide; ODM; virucide; vaccine; Paramycviridae; F protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.
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Pred. No. 21;
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                                                                                                 Klinman DM;
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Best Local Similarity 100.0%;

Matches 20; Conservative 0,
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               07-JUN-2001; 2001WO-US018276
                                        07-JUN-2000; 2000US-0209797P
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01-SEP-2000; 2000US-0229307P.
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                                                                       (BIOS+) BIOSYNEXUS INC.
                                                                                                                              WPI; 2002-130570/17,
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                                                                                                 Flora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200211761-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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                                                                                                                    The invention describes a vaccine comprising one or more epitopes of a bramyxoviridae P protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond) -oligodideoxynucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral broncholitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been barticularly implicated in death of infants that are premeture, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type
Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxymucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CpG oligodeoxynucleotide D29 used for dendritic cell maturation.
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/*tags a THER
/mod_base= OTHER
/note= "OTHER= phosphorothioate nucleotides"
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/mod_base= OTHER
/note= "OTHER= phosphorothioate nucleotide"
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
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The present sequence is that of a CpG oligodeoxynucleotide of the invention. A claimed method for generating dendritic cells involves contacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxynucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dendritic cell; tumour; immunotherapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.
                                                                  The present sequence is that of D type CpG oligodeoxymucleotide D29, which is used in a claimed method for generating a mature dendritic cell The method involves contacting a dendritic cell precursor, especially a monocyte, with the oligonucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                                                                                                                     Score 20; DB 7; Length 20; Pred. No. 21;
                                                                                                                                                                                                                                                                                     Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
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                                  Claim 11; Page 44; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                  1 GGTGCACCGGTGCAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                         100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002; 2002WO-US025732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC48313 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CpG oligodeoxynucleotide;
                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
Les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CpG oligodeoxymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gursel M,
cligodeoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-300874/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC48313;
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC48313
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to treat diseases such as cancer. Mature dendritic cells may also I to produce activated T lymphocytes

system to

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Gaps

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Indels

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The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilising agent and encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing growth of a solid tumour cell (e.g. human tumour cell) bearing an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an immune response against tumours or stimulating an invito or an in vitro immune cell, and for inducing an immune response against an in vitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxynucleotides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, francisella, schistosomiasis, tuberculosis and leishmaniasis, cancer etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever, bronchial or allergic asthma, urticaria, food allergies), autoimmune condiseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and multiple sclerosis) and psoriasis. The present sequence is a D class CpG CDN potentially useful for encapsulating in SSCL
                                                                                                                                                                                                                                                                                                                                                                                                                             oligodeoxynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sterically stabilised cationic liposome; SSCL, ODN; oligodeoxymucleotide tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour; thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis; CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; ss.
                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                    D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
                                                                                ..
                                         7; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joshi BH,
                                                                                0; Indels
BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawakami K,
                                      Score 20; DB
Pred. No. 21;
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishii KJ,
                     100.0%; Scc.
100.0%; Pre
                                                                                                                    20
                                                                                                                                                         1 GGTGCACCGGTGCAGGGGG 20
                                                                                                                       1 GGTGCACCGGTGCAGGGGGG
                                                                                                                                                                                                                                                                 ACC83118 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2002; 2002WO-US024235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-2001; 2001US-0308283P.
25-JUL-2002; 2002US-00206407.
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klinman DM, Gursel I,
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                                                          Local Similarity
les 20; Conser
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                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
    Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2003.
                                                                                                                                                                                                                                                                                                      ACC83118;
                                         Query Match
                                                                                Marches
                                                                                                                                                                                                                          RESULT 11
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The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a collipid, stabilising agent and encapsulating a K type oligodeoxymucleotie (ODN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing an immune relation. The invention is useful in pharmaceutical composition for impairing an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an invito immune cell, and for inducing an immune response against an in vitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxymucleotides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxymucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic liposome composition for delivering oligodeoxynuclectides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour; thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis; CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puri RK;
                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                           sequence useful for encapsulating in SSCL, D29.
                                       Score 20; DB 8; Length 20; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Joshi BH,
                                                                               Indels
Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                               ö
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                                   y Match
Local Similarity 100.0%; Score 20; DB
Local Similarity 100.0%; Pred. No. 21;
hes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                    1 GGTGCACCGGTGCAGGGGGG
                                                                                                                                           1 GGTGCACCGGTGCAGGGGGG
                                                                                                                                                                                                                                                        ACC83152 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2002; 2002WO-US024235.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                   27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                           class ODN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2003
                                                                                                                                                                                                                                                                                              ACC83152;
                                       Query Match
                                                                             Matches
                                                                                                                                                                                                                  RESULT 12
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The present invention describes a method for inducing the production of vascular endothelial growth factor (VBGP) by a cell comprising contacting the cell with a CpG oligonucleotide and therefore inducing the production of VBGP by the cell. Also described: (1) inducing neovascularisation in a tissue, comprising introducing a CpG oligonucleotide into an area of the tissue, comprising introducing a CpG oligonucleotide into an area of the tissue, and so inducing neovascularisation in the area of the tissue, (2) promoting angiogenesis in an area of the subject; where angiogenesis is desired, angiogenesis in an area of the subject; where angiogenesis and sea of the subject where angiogenesis in the subject; and (3) screening for an agent that inhibits neovascularisation, comprising angiogenesis in the subject; and (3) screening for an agent that inhibits neovascularisation, comprisation the past to the animal indicates that the mammal, where inhibition of angiogenesis in the animal indicates that the mammal, where inhibition of angiogenesis in the animal indicates that the agent is effective in inhibiting neovascularisation. The CpG oligonuclectides have vulnerary, vasotropic and antiarteriosclerotic activities, and can be used in inducing angiogenesis or cliganuclectides can be used in inducing angiogenesis or cliganuclectides can be used in inducing angiogenesis or subjects who have a wound or who have
                                                                                                                                                                                            ..
bronchial or allergic asthma, urticaria, food allergies), autoimmune diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and multiple sclerosis) and peoriasis. The present sequence is a D class ODN potentially useful for encapsulating in SSCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing the production of vascular endothelial growth factor by a cell, useful for inducing angiogenesis, comprises contacting the cell with a CpG oligodeoxynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular endothelial growth factor; VEGF; CpG oligonucleotide; necovascularisation; anglogenesis; vulnerary; vasotropic; anglogenesis; antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
                                                                                                                                                                                            ö
                                                                                                                                                   100.0%; Score 20; DB 8; Length 20; 100.0%; Pred. No. 21;
                                                                                                                                                                                              Indels
                                                                                                        Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                              ö
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYTE-) UNIV TENNESSEE RES CORP.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; SEQ ID NO 13; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D oligonucleotide SEQ ID NO:13.
                                                                                                                                                                                                                                       1 GGTGCACCGGTGCAGGGGG 20
                                                                                                                                                                                                                                                                             1 Gerecacceerscaeces 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rouse BT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis; ischaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2002; 2002WO-US040955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DBC-2001; 2001US-0343457P.
                                                                                                                                                                                                                                                                                                                                                                                   ADD01049 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                Conservative
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                                                                                                                                     Query Match
Best Local Similarity
Marches 20; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                               ADD01049;
                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                    ADD01049
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an immunostimulatory oligonucleotide described in the exemplification
                  the invention
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                   Key
misc_RNA
                                                                                                                                                                                                                           ABL35603;
                                                                                        Matches
                                                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies). Lyme disease, hepatitis, HIV or malariai. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
atherosclerosis or ischaemia. The method may also be used in screening for agents that inhibit neovascularisation. The present sequence represents a CpG oligonucleotide which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 28
/*teg= a
/notionally thymidine is replaced by uracil to
/note= "optionally thymidine is replaced by uracil to
floom RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar*
                                                                                                                                                                                                                                                                                                                        DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
                                                                                                                                                                                                                                                                                                                                   infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacde; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or
                                                                                                               Gaps
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                                                                                        9; Length 20;
                                                                                                              Indels
                                                               Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                               ;
                                                                                                                                                                                                                                                                                                  Immunostimulatory oligonucleotide SEQ ID NO: 525.
                                                                                     Score 20; DB
Pred. No. 21;
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page 61; 68pp; English.
                                                                                                                                       1 GGTGCACCGGTGCAGGGGG 20
                                                                                                              ..
                                                                                                                                                             GGTGCACCGGTGCAGGGGG 20
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                                                                                      100.0%;
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                                                                                                                                                                                                                         ABL35599 standard; DNA; 28
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOS-) BIOSYNEXUS INC.
                                      the present invention
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                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200193902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV infection
                                                                                                                                                                                                                                                                           04-APR-2002
                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                         Key
misc_RNA
                                                                                                                                                                                                                                                  ABL35599;
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                                                                                                 Best Loc
Matches
                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                              ABL35599
  88888
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comprises at least one oligonucleotide comprising both an RNA region and an DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note="optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunostimulatory compositions comprising RNA/DNA hybrid obligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimulantusuppressive; protozoacie; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
                                                                                                                                Gaps
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                                                                                                                                ..
                                                            6; Length 28;
                                                                                                                             0; Indels
10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunostimulatory oligonucleotide SEQ ID NO: 529.
                                                            Score 20; DB
Pred. No. 21;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 28
/*tag= a
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                                                                                                                                                                                                                                            GETGCACCGGTGCAGGGGGG 20
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                                                            100.0%;
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                                                                                                                                20; Conservative
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                                                            Query Match
Best Local Similarity
Sequence 28 BP;
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XX SQ . Sequence 28 BP; 4 A; 6 C; 13 G; 5 T; 0 U; 0 Other;

0; Gaps Query Match 100.0%; Score 20; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 21; Matches 20; Conservative 0; Mismatches 0; Indels

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Search completed: July 2, 2004, 08:31:32 Job time: 149.878 secs

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July 2, 2004, 08:09:30 ; Search time 31.3415 Seconds (without alignments) 354.132 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
Sequence:
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

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Issued\_Patents NA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Appli	2752, Ap	, Appli	Appli	2, Appl	42, Appl	5836, Ap	5639, Ap	5555, Ap	5590, Ap	20, Appl	24, Appl	4, Appl	, Appli	Appli,	Appli	, Appli	Appli	2, Appli	1, Appli	, Appli	81, Appl	07, App	, Appli	Appli	Appli	, Appli
Description	Sequence 1			Sequence 2		Sequence 4							Sequence 2	Sequence 1	Sequence 1	Sequence 1	Sequence 3	Sequence 6	Sequence	Seguence	Sequence 3	Sednence 8	Seguence 2	Seguence 4	Seguence 2	Sequence 2	Sequence 1
QI	US-09-922-445-1	US-09-489-039A-2752	US-09-248-571-2	US-09-553-736-2	US-08-060-925A-12	US-09-328-925-42	US-09-489-039A-5836	US-09-252-991A-5639	US-09-252-991A-5555	US-09-252-991A-5590	US-09-655-270A-20	US-09-651-941-24	US-09-955-597-24	US-09-655-270A-1	US-09-651-941-1	US-09-955-597-1	US-09-740-027-3	US-09-146-053-6	US-09-103-840A-2	US-09-103-840A-1	US-08-959-381A-3	US-09-170-496D-81	US-09-170-496D-207	US-08-959-381A-4	US-08-687-289A-2	US-09-435-897-2	US-08-041-538-1
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US-08-463-642-1 US-08-455-602-1	US-08-465-157-1 PCT-US91-09422-1	PCT-US91-09422-16 US-08-976-259-73	US-09-313-294A-385	US-09-023-655-668	US-09-422-869-19	US-09-916-510A-18	US-09-342-681C-107	US-09-621-976-18710	US-09-016-434-714	US-09-833-381-1374	US-08-469-667-6	US-09-224-110-6	PCT-US95-07289-6
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74.0 4300 5 74.0 4300 5 74.0 6336 4 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 2194 1 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 22.0 22.0 3 72.0 2 72.	PCT-US31-09422-1 PCT-US31-09422-1 US-08-976-259-73 US-09-313-294A-385 US-09-313-294A-385 US-09-313-655-668 US-09-422-869-19 US-09-422-869-19 US-09-342-68LC-107 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870 US-09-621-976-1870	ALIGNMENTS 445 D METHODS FOR DETE 09/922,445 3 24801 is a single 24941 is a single
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Sequence 2752, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: PREDUNONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF ILLING DATE: 2000-01-27

CURRENT FILLING DATE: 2000-01-27

PRIOR PILLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 2752

LENGTH: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09248571

Sequence 2, Application US/09248571

Fatent No. 6136539

GENERAL INFORMATION:

APPLICANT BASBAUM, CARCL

APPLICANT GALLUP, MARIANB

APPLICANT GALLUP, MARIANB

APPLICANT GENERAL SERV

APPLICANT GENSCH, ERIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5-MUCIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5-MUCIN

TITLE OF INVENTION: QENE EXPRESSION

TITLE OF INVENTION: QENE EXPRESSION

TITLE OF INVENTION WHERE: 1999-02-11

EARLIER APPLICATION NUMBER: 60/074,398

EARLIER APPLICATION NUMBER: 60/074,398

EARLIER APPLICATION NUMBER: 22

SOFTWARE: PALENTH VET. 2.0

SOFTWARE: PALENTH VET. 2.0

SOFTWARE: PALENTH VET. 2.0

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SOFTWARE: PALENTH VET. 2.0
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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Pred. No. 1.6e+02;
0; Mismatches 2;
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US-09-553-736-2

Sequence 2, Application US/09553736

Patent No. 6446672

GENERAL INFORMATION:
APPLICANT: BASBAUM, Carol
APPLICANT: GALLOP, Marianne
APPLICANT: GREEMICHAEL, Assefa
APPLICANT: GREEMICHAEL, Assefa
APPLICANT: GREEMICHAEL, Assefa
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: MUCIN GENE EXPRE
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                                                                                                                                                                                                                                                                                                                                             TYPE: DNA; Clebsiella pneumoniae; ORGANISM: Klebsiella pneumoniae
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89.5%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2
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US-09-248-571-2
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LOCATION: (32529) .(33414)
LOCATION: (32529) .(33414)
NAME/KEY: misc feature
LOCATION: (32614) ..(32614)
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be OTHER INFORMATION: A or G
                                                                                                                                                                                                                                                                                                                                                                                      DOCATION: (31748)..(31841)
OTHER INFORMATION:
NAME/FEY: Intron
UCACTION: (31842)..(32400)
OTHER INFORMATION:
NAME/FEX: MAISC feature
NAME/FEX: MAISC feature
OTHER INFORMATION: Malectide 32163 is a single nucleotide polymorphism which can be OTHER INFORMATION: A or C
NAME/FEX: exon
LOCATION: (3250)..(32528)
OTHER INFORMATION: (32528)
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          (27645)..(27645)
RMATION: nucleotide 27645 is a single nucleotide polymorphism which can
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90.0%; Pred. No. 57;
tive 0; Mismatches
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PUBLICATION INFORMATION:
DATHBASE ACCESSION NUMBER: Genbank/AC004923
DATHBASE BUTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1).(38653)
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OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (36524)..(38341)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (38452)
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Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                   LOCATION: (30520)..(30681)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (30682)..(30894)
OTHER INFORMATION:
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LOCATION: (30895)..(31027)
OTHER INFORMATION:
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LOCATION: (31028)..(31747)
OTHER INFORMATION:
                              OTHER INFORMATION: nucleot
OTHER INFORMATION: C or G
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COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-S MUCIN GENE EXPRESSION

RESULT 2 US-09-489-039A-2752

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5816, Application US/09489039A

Sequence 5816, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PAILOR DATE: 1999.01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 5836

LENGTH: 366
                                                                                                                                                    RESULT 6
US-09-328-925-42
US-09-328-925-42
| Sequence 42, Application US/09328925
| Patent No. 6610906
| GENERAL INFORMATION:
| APPLICANT: Kurachi, Sumiko
| TITLE OF INVENTION: Nuclectide Sequences for Gene Regulation and Methods of
| TITLE OF INVENTION: Unclectide Sequences for Gene Regulation and Methods of
| TITLE OF INVENTION: UNGERTION: UNGERTION NUMBER: US/09/328,925
| CURRENT PILING DATE: 1999-06-09
| NUMBER OF SEQ ID NOS: 84
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 42
| LENGTH: 12222
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels 0
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; Sequence 5639, Application US/09252991A
; Patent No. 6551795
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         1 GGTGCACCGGTGCAGGGGG
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Pest Local Similarity 94.1%;
Matches 16; Conservative
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, ORGANISM: Homo sapiens
US-09-328-925-42
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GENERAL INCOMPATION

1. Sequence 12. Application US/08060925A

Patent No. 5438824

GENERAL INCOMPATION

TITLE OF INVENTION INCREASED EXPRESSION OF ALPHA-1

TITLE OF INVENTION INCREASED EXPRESSION VECTORS THROUGH THE INCLUSION OF

TITLE OF INVENTION INCREASED EXPRESSION VECTORS THROUGH THE INCLUSION OF

TITLE OF INVENTION INCREASED EXPRESSION VECTORS THROUGH THE INCLUSION OF

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TITLE OF INVENTION INCREASED EXPRESSION OF ALPHA-1

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TITLE OF INVENTION INCREASED EXPRESSION OF ALPHA-1

CORRESSED EXPORTED TO THE OFFICE OF ALPHA-1

STATES CONTINUER: INCREASED EXPRESSION OF ALPHA-1

COMPUTER: LEAR PACTOR TO THE OFFICE O
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
79.0%; Score 15.8; DB 4; Length 3358;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0
FILE REFERENCE: UCSF-012/03US
CURRENT APPLICATION NUMBER: US/09/553,736
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/074,398
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEROTH: 3358
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Best Local Similarity 89.5%;
Matches 17; Conservative C
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-553-736-2
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US-09-652-70A-20

1 Sequence 20, Application US/09655270A

2 Sequence 20, Application US/09655270A

3 Sequence 20, Application US/09655270A

4 Patent No. 6329151

5 Patent No. 6329151

5 PATILE NEPRHATION: High Density Sampling of Differentially Expressed Prokaryotic

7 TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic

8 FILE REFERENCE: BC1011 US NA

9 CURRENT APPLICATION NUMBER: US/09/05

9 FILE REFERENCE: 1999-February-19

9 FILE PRICE PRICE DATE: 1999-February-19

9 FILE PRICE PRICE DATE: 1999-February-19

9 RIOR FILING DATE: 1999-September-03

NUMBER: OF SEQ ID NOS: 37

9 SOFTWARE: Microsoft Office 97

1 SEQ ID NO 20

1 LENGTH: 1083
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Best Local Similarity 85.0%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0
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US-09-252-991A-5555/C
is Sequence 5555, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGMOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGMOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PLING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5555
SEQ ID NO 5555
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| Sequence 5590, Application US/09252991A |
| Sequence 5590, Application US/09252991A |
| Parent No. 6587198 |
| GENERAL INFORMATION |
| APPLICANT MARC U. Rubenfield et al. |
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| CURRENT PILING DATE: 1999-02-18 |
| PRIOR FILING DATE: 1999-02-18 |
| PRIOR PLING DATE: 1998-02-18 |
| PRIOR PLING DATE: 1998-07-27 |
| NUMBER OF SEQ ID NOS: 33142 |
| SEQ ID NO 5590 |
| LENGTH: 774 |
| LENGTH: 775 |
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Pred, No. 3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5639
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-5639
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ORGANISM: Pseudomonas aeruginosa
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-5590
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85.0%;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
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US-09-252-991A-5555
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PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 12523
TYPE: DNA
ORGANIEM: Rhodococcus erythropolis HL PM-1
US-09-651-941-1
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Job time : 36,3415 secs
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US-09-655-270A-1

| Sequence 1, TITLE 06 INVENTION: High Density Sampling of Differentially Expressed Prokaryotic mR TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic mR FILE REFERENCE: BC1011 US NA CURRENT APPLICATION NUMBER: US/09/655,270A CURRENT FILING DATE: 1999-February-19
PRIOR PRILING DATE: 1999-February-19
PRIOR PRILING DATE: 1999-February-19
PRIOR FILING DATE: 1999-September-03
NUMBER OF SEQ ID NOS: 37
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 1
| LENGTH: 12508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.0%; Score 15.2; DB 4; Length 1098; Best Local Similarity 85.0%; Pred. No. 3e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0
                 ## Sequence 24, Application US/09955597
| Patent No. 6461856
| Patent Can'r Rouvier, Dana Maliers, Dana Maliers, Dana Maliers, Dana Maliers, Dana Maliers, Dana Mappilcantown: Rainer, Russ
| TITLE OF INVENTION: Genes Encoding Picric Acid Degradation FILE OF INVENTION: Genes Encoding Picric Acid Degradation
| FILE REPERENCE: BC10.22 US NA CURRENT APPLICATION NUMBER: 60/152,545
| PRIOR PILING DATE: 1999-10-03 NUMBER OF SEQ ID NOS: 28 |
| SOFTWARE: Microsoft Office 97 |
| SEQ ID NO 24 |
| LENGTH: 1098 |
| TYPE: DNA |
| TYPE: DNA |
| GRANISM: Rhodococcus erythropolis HL PM-1 US-09-955-597-24
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Patent No. 6355470
GENERAL INFORMATION:
APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: RAINENS, DANA M
TITLE OF INVENTION: Genes Encoding Picric Acid Degradation FILE REFERENCE: BC1022 US NA
CURRENT APPLICANT NUMBER: US/09/651,941
CURRENT FILING DATE: 2000-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rhodococcus erythropolis HL PM-1
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US-09-955-597-24
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US-09-651-941-1
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) OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-496
                                                                                                                                                                                                                                                                                                                                                                  Sequence 456, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: TILINAN, DENNIS M.
TILLE OF INVENTION: IMMUNOSTIMILATORY RNA/DNA HYBRID MOLECULES
FILE REFRENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: 05/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
US-09-874-991C-499

US-09-874-991C-506

US-09-874-991C-516

US-09-874-991C-543

US-10-068-160-38

US-10-068-160-38

US-10-068-160-37

US-10-068-160-37

US-10-98-74-991C-516

US-09-874-991C-528

US-09-874-991C-528

US-10-66-022-2

US-10-66-022-2

US-10-68-160-13

US-10-68-160-14

US-10-068-160-54

US-10-068-160-54

US-10-068-160-54

US-10-068-160-54

US-10-068-160-54

US-10-068-160-60

US-10-194-035-37

US-10-194-035-37
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Publication No. US20040052763A1
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ORGANISM: Artificial Sequence
  RESULT 2
US-09-874-991C-504
; Sequence 504, Appl
; Publication No. US
                                                                                                                                                                                                                                                                                                                                                          US-09-874-991C-496
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LENGTH: 20
 Query Match
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Matches
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Sequence 504, App
Sequence 517, App
Sequence 510, App
Sequence 540, App
Sequence 42, Appl
Sequence 178, App
Sequence 517, App
Sequence 529, App
Sequence 529, App
Sequence 529, App
Sequence 529, App
Sequence 539, App
Sequence 539, App
Sequence 539, App
Sequence 548, App
Sequence 548, App
                                                              2, 2004, 08:11:05; Search time 154.146 Seconds (without alignments) 625.926 Million cell updates/sec
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                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-874-991C-504
US-09-874-991C-504
US-09-874-991C-540
US-10-068-160-2
US-10-068-160-2
US-10-666-022-178
US-09-874-991C-525
US-09-874-991C-525
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
US-09-874-991C-537
                                                                                                                                                                                         hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Length 20; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507
APPLICANT: FLORA, MICHABE,

APPLICANT: KLINMAN, DENNIS M.

TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFRENCE: 07787.0642-0

CURRENT APPLICATION NUMBER: 0020-06-07

PRIOR APPLICATION NUMBER: 60209,797

PRIOR APPLICATION NUMBER: 6020-06-07

NUMBER OF SEQ ID NOS: 620

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 504

LENGTH: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 371, Application US/09874991C

Publication No. US20040052763A1

GENERAL INFORMATION:

APPLICANT: MOND, JAMES J.

APPLICANT: FLORA, MICHAEL

APPLICANT: FLORA, MICHAEL

APPLICANT: FLORASTING NOWBER: US/09/874,991C

CURRENT APPLICATION NUMBER: US/09/874,991C

CURRENT APPLICATION NUMBER: 60/209,797

PRIOR APPLICATION NUMBER: 60/209,797

PRIOR PILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 620

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 507
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APPLICANT: ELORA, MICHAEL
APPLICANT: ELORA, MICHAEL
APPLICANT: KILNMAN, DERNISS M.
ITILE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 13; Length 20;
Pred. No. 9.9;
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100.0%; Score 20; DE
Best Local Similarity 100.0%; Pred. No. 9.9
Matches 20; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 20; Conserv
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GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVERTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE FILE REPRENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRICR APPLICATION NUMBER: 60/128,898
PRICR PLILING DATE: 1999-04-12
NUMBER OF SEO ID NOS: 120
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 540, Application US/09874991C
| Publication No. US20040052763AL
| GENERAL INFORMATION:
| APPLICANT: MOND, JAMES J.
| APPLICANT: RIORA, MICHAEL
| APPLICANT: KLINNAN, DENNIS M.
| TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
| FILE REFERENCE: 07787.0042-0
| CURRENT APPLICATION NUMBER: US/09/874,991C
| CURRENT APPLICATION NUMBER: 00/209,797
| PRIOR FILING DATE: 2001-06-07
| PRIOR FILING DATE: 2000-06-07
| NUMBER OF SEQ ID NOS: 620
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Pred. No. 9.9;
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Pred. No.
                             /209,797
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Publication No. US20030060440A1
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
CURRENT FILING DATE: 2001-06-0
PRIOR PILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
ESO ID NO 514
LENGTH: 20
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                               ORGANISM: Artificial Sequence
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SEQ ID NO 540
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MOND, JAMES J.

TITE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07087 -0042-0

CURRENT APPLICATION NUMBER: US/09/874,991C

CURRENT PILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 620

SOFTWARE: PALENTIN WORD: 2.1

SEQ ID NO 517

LENGTH: 28
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| Sequence 525, Application US/09874991C
| Publication No. US20040052763A1
| GENERAL INFORMATION:
| APPLICANT: MOND, JAMES J.
| APPLICANT: RIGHA, MICHARL
| APPLICANT: KLIWAN, DENNIS M.
| TITLE OP INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
| PILE REFERENCE: 07787.0042-0
| CURRENT APPLICATION NUMBER: US/09/874,991C
| CURRENT APPLICATION NUMBER: 60/209,797
| PRIOR FILING DATE: 2001-06-07
| NUMBER OF SEQ 1D NOS: 620
| SEQ 1D NO 525
| LENGTH: 28
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Pred. No. 9.9;
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Pred. No. 9.5;
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Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                    TYPE: DNA

ORGANISM: Artificial Sequence

FRATURE:

OTHER INPORMATION: Synthetic

US-10-666-022-178
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     LENGTH: 20
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Sequence 178, Application US/10666022

Sequence 178, Application US/10666022

Publication No. US20040105872A1

Sequence 178, Application No. US20040105872A1

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services

APPLICANT: Werthelyi, Daniela

TITLE OF INVENTION: METHOO OF TREATING AND PREVENTING INFECTIONS IN INMUNOCOMPROMISE

TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

TITLE PREPRENCE: 4239-66899

CURRENT APPLICATION NUMBER: US/6699

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: US 60/411,944

FRIOR PILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 181

SEQ ID NO 178
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7

US-10-194-035-42

US-10-194-035-42

Sequence 42, Application US/10194035

Publication No. US200314422941

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KINNAN, Dennis
APPLICANT: SHII, Ken
APPLICANT: WERTHELYI, Daniela
TITLE OF INVENTYON: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT PILLING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1

LENGTH: 20
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42
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100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                    ) OTHER INFORMATION: Oligonucleotide US-10-068-160-2
                                                                                                                                                                                                                                                                                                                        1 GGTGCACCGGTGCAGGGGGG 20
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                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
SEQ ID NO 2
LENGTH: 20
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-495
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US-09-874-991C-548
                                                                                                                          Sequence 548, Application US/09874991C
| Publication No. US20040652763A1 |
| General Information No. US20040652763A1 |
| General Information No. US2004065763A1 |
| APPLICANT: MICHAEL J. |
| APPLICANT: FICRA, MICHAEL MICHAEL |
| APPLICANT: KIINMAN, DENNIS M. |
| TITLE OF INVENTION: INMUNOSTRUILATORY RNA/DNA HYBRID MOLECULES |
| FILE REFERENCE: 07787.0042.0 |
| CURRENT APPLICATION NUMBER: US/09/874,991C |
| CURRENT FILING DATE: 2001-06-07 |
| PRIOR FILING DATE: 2001-06-07 |
| NUMBER OF SEQ ID NOS: 620 |
| SOFTFARE: Patentin Ver. 2.1 |
| SEQ ID NO 548 |
| LENGTH: 40 |
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APPLICANT: FLORA, MICHABL
APPLICANT: FLORA, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPREMENT: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 495, Application US/09874991C Publication No. US20040052763A1 GENERAL INFORMATION:
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PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 495
LENGTH: 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 20; Conservat
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US-09-874-991C-499
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US-09-874-991C-495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-529
                                                                                                                                                                                                                                                                                                                                                           Sequence 529, Application US/09874991C

Publication No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: FLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 2010-06-07
CURRENT FILING DATE: 2011-06-07
PRIOR APPLICATION NUMBER: 06/209,797
PRIOR APPLICATION NUMBER: 66/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOUTHMER: Patentin Ver. 2.1
SEQ ID NO 529
LENGTH: 28
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Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOUD JAMES J.
APPLICANT: KLINAMA, DENNIS M.
TITLE OF INVENTION: IMMENS: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR PILICATION NUMBER: 05/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 6200
SOUTHARE OF SEQ ID NOS: 6200
SOUTHARE OF SEQ ID NOS: 6200
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100.0%; Score 20; DB 13; Length 28; larity 100.0%; Pred. No. 9.5; Conservative 0; Mismatches 0; Indels
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Pred. No. 9.5;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 20, Conservative
Query Match
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APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KILDMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT PILING DATE: 2004-06-07
PRIOR PLLING DATE: 2004-06-07
PRIOR PLLING DATE: 2000-06-07
PRIOR PLLING DATE: 2000-06-07
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 499
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
PRATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-499
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CC109078 NDL.50B23
AL269542 Tetracdon
BX426076 BX426076
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BF582545 602094520
AL292797 Tetracdon
B1334719 602999611
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Hedyotis terminalis
Bukaryota; Viridintae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentlanales; Rubiaceae; Rubioideae;
Spermacoceae; Hedyotis.
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Expressed tag sequences from Hedyotis terminalis flower - Stage 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: W. Richard McCombie
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fal: 516 367 8884
Fax: 516 367 8874
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BB45626
AV219401
BY103614
AL898002
BZ782509
CE182406
AL897989
BZ422920
CE284352
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BJ252893
BE973745
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CE419868
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DEFINITION
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KEYWORDS
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AUTHORS
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COMMENT
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Maximum Match 100%
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10: gb_est1:*
11: gb_est2:*
12: gb_est3:*
13: gb_est4:*
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Hedyotis centranthoides
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Magnoliophyta; endicotyledons; core eudicots;
Spermatochae; Rentjanales; Rubiaceae; Rubioideae;
Spermacochae; Hedyotis.

[ (bases 1 to 509)
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Expressed tag sequences from Hedyotis centranthoides flower - Stage
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Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHI 12/21/01 Library: Strategene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enz
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"
for large inserts. Sample: collected on the island of Hawaii, Hawaii, NYBG herbarium voucher TM2563"
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/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
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Pred. No. 3.38+03;
0; Mismatches 1; Indels 0;
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Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Bazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Fax: 214313UnivRev
High quality sequence stop: 509.
Location/Qualifiers
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                                                                                      Query Match 92.0%; Score 18.4; DB 14;
Best Local Similarity 95.0%; Pred. No. 3.3e+03;
Matches 19; Conservative 0; Mismatches 1;
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l Similarity 95.0%;
19; Conservative 0
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CB087525/c
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/note="Corpan: flower; Vector: pBK-CNV; Site 1: Xho!;
Site 2: Ecc R! Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express CDNA
Sythesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"
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Hedyotis centranthoides
Hedyotis centranthoides
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacoceae; Hedyotis.
Spermacoceae; Hedyotis.

I (bases 1 to 440)
Levesque, M.P., Twigg, R.M., Motley, T., Katari, M.S., Dedhia, N.N.,
O'shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Empressed tag sequences from Hedyotis centranthoides flower - Stage
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Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tal: 516 367 8884
Pax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.0%; Score 18.4; DB 14; 95.0%; Pred. No. 3.2e+03;
                                                                                                                     1. .339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                         /mol_type="mRNA"
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Plate: hj98 row: g column: 11
Seg primer: -21Mi3UnivRev
High quality sequence stop:
Location/Qualifiers
                        Plate: hf37 row: c column: 06
Seg primer: -21M3UnivRev
High quality sequence stop: 339,
Location/Qualifiers
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mccombie@cshl.org
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CB087291.1 GI:27911483
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Best Local Similarity
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CB087291/c
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REFERENCE AUTHORS

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LSM mays subsp. mays (maize)

Zea mays subsp. mays

Everatory as subsp. mays

Grade; Panicoideae; Andropogoneae; Zea.

I (bases 1 to 610)

S Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.

Sequencing of the maize genome

Unpublished (2003)

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG692380 610 bp DNA linear GSS 14-OCT-2003
ZMMBBb0292G11.f ZMMBBb Zea mays subsp. mays genomic clone
ZMMBBb0292G11 5', genomic survey sequence.
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                                                                                                                                                                                                                                                          1. .840.
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/db_xref="taxon:4577"
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/clone="law="zea" or 1:5-KB"
/note="vector: pBGSK-; Site 1: HincH; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 840;
                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA 11: 301-838-5643
Fax: 301-838-6208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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Best Local Similarity 95.0%; Pred. No. 3.5e+03;
Matches 19; Conservative 0; Mismatches 1;
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/mol type="genomic DNA"
/cultivar="B73"
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Seg primer: T7
Class: BAC ends.
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        Other_GSSs: OGODZ26TH
Contact: Cathy Whitelaw
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BACKWARD: M13r
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CG692380
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Hedyotis centranthoides
Hedyotis centranthoides
Beatranthoides
Spermacocata; Varidiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermacocae; Hedyotis;
Spermacocae; Hedyotis.

1 (bases 1 to 598)
Levesque, M. P., Twigg, R. W., Motley, T., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.

Expressed tag sequences from Hedyotis centranthoides flower - Stage
hk03f05.gl Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis centranthoides CDNA clone hk03f05, mRNA sequence. CB087525.1 GI:27911717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: flower; Vector: pBX-CMV; Site 1: XhoI; Site_2: Eco RI; Date: Completed 12/18/01. Submitted to CSHI 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Xit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii, NYBG herbarium voucher TM2563"
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B40 bp DNA linear GSS 25-AUG-2003
CG022GTV ZM 0.7 1.5 KB Zea mays genomic clone ZMVBMa0696F04,
GG271799.1 GI:34183940
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1 (Dases 1 to 840)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Click, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for waize Genomics
Unpublished (2002)
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/clone_lib="Hedyotis centrantholdes flower - Stage 2
(NYBG)"
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                                                                                                                                                                                                                                                                                                                                                                                                          2 (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Eax: 516 367 8874
Email: mccombieGeshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: hk3 row: f column: 05
Seq primer: -21M13UnivRev
High quality sequence stop: 598.
Location/Qualifiers
1. 598
//organism="Hedyotis centranthoides"
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//clone="hk01605"
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Zea mays
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RESULT 5 CG271799 LOCUS DEFINITION

ORIGIN

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ACCESSION

REFERENCE AUTHORS

TITLE

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Gaps

ORIGIN

RESULT 7 CC109078/c LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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Location/Qualifiers

1. 799
| organism="Aedes aegypti"
| formula |
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Stegomyia.

Stegomyia.

1 (Dases 1 to 799)

Inftus, B., Shetty, J., Knudson, D. and Severson, D.

BAC end Sequencing of Aedes aegypti
Unpublished (2003)

Other_GSSs: NDL.50B22.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TiGR
9712 Medical Center Drive, Rockville, MD 20850, USA
TiGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-524
Fax: 301-838-526
Email: entactigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
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Actinopterygii, Neopterygii, Teleostei, Enteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location-Qualifiers

/ organism="Abedes aegypti"

/ stain=#liverpool"

/ db_xref="taxon:7159"

/ clone="Nucre Dame Liverpool"

/ clone="Nector: pBCBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
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NDL.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone NDL.50B22, genomic survey sequence.
CC133230
CC133230.1 GI:30002285
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Bukaryotic Genomics
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA
7121: 301-838-0308
Fax: 301-838-0208
Email: enca@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
                                                                                                       Query Match
Best Local Similarity 94.7%; Pred. No. 8.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels
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1 (bases 1 to 779)

Loftus, B., Shetry, J., Kmudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)

Other GSSs: NDL, 50B23.SP6

Contact: Brendan Loftus
                 ssp. mays"
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Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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Aedes aegypti
       HindIII, Zea mays L.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

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/organism="Howo sapiens"
/nol_type="mRNA"
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5', mRNA sequence.
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AV393217.1 GI:6547433
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1 (bases 1 to 1214)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2501 row: a column: 06
High quality sequence stop: 150.
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Pred. No. 8.8e+03;
0; Mismatches 1; Indels 0;
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Matches 18; Conservative 0
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Gondact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Prance
BP 191 91006 EVRY cedex - Prance
BMail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. This sequence belongs to sequence cluster 1373.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOAAWISZA080Pl&cluster=1373.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fullibegth.invitrogen.com/ InvitroGen Corporation 1600
Faradday Avenue Genoscope sequence ID : CSOAAWISZA08QPl.
                                              Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 1919 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

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/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6, 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/note="Genoscope sequence ID : C0BG073BH09SP1~end
PUC-Or1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db_zref="taxon:99883"
/clone="073018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.4; DB 29;
Pred. No. 8.7e+03;
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94.7%; Pred. No. b...
... 0; Mismatches
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mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF009YC20"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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                                (bases 1 to 1005)
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Best Local Similarity 94.75
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BX426076
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High quality sequence stop: 237.
Location/Qualifiers
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Mus musculus (house mouse)
Mus musculus
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90.0%;
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Best Local Similarity
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1 (Dases 1 to 142)

1 (Dases 1 to 142)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Unpublished (1999)

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

5 Email: cgapba-remail.nih.gov

7 Tissue Procurement: ATCC

5 CDNA Library Preparation: Ling Hong/Rubin Laboratory

6 CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LIML)

7 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

8 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

8 High quality sequence start: 2

9 High quality sequence start: 2
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                                                                                                                                                                                                                                                                                                                                   Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                      Chlamydomonadacee; Chlamydomonas.

1 (bases 1 to 354)

Asamitut.E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433

DNA Res. 6 (6), 369-373 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
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/clome="CMO7f03"x"
/dev_stage="photoautotrophic growth"
/clome="Wector: pBluescriptII SK-; Site_1: EcoRI; Site_2: AhoI
                                                             Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                            Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
SST.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
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BE388878
BE388878.1 GI:9334243
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Homo sapiens
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KEYWORDS
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. T. (Dases 1 to 237)

18. (Dases 1 to 237)

20. (Dases 1 to 237)

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/Lissue_type="endometrium, adenocarcinoma cell line"
/Lis host="PHIOB (phage-resistant)"
/clone lib="NHH MGC 44"
/note="Organ: uterus, Vector: pOTB7; Site_1: Xho1; Site_2:
EcoR1; DNA made by oligo-dr priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M: Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 80.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rry; Purified genomic DNA from M.
musculus C578L/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 10; Length 142;
Pred. No. 1.3e+04;
0; Mismatches 2; Indels 0;
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Fax: 801 585 7177
Email: dounnegemetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0326 row: G column: 23
Seq primer: CGTFGTAAAACGACGGCCAGT
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/organism="Mus musculus"
/nol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0326G23"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 275)

Konno,H., Aizawa,K., Akahira; S., Akiyama,J., Arakawa,T.,

Garninoi,P., Budo,T., Fukuda,S., Pukuishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishi,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyoswa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,

Kusakabe,M., Mateuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,

Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,

Sogabo,Y., Sugahara,Y., Shigemoto,Y., Wataniki,A.,

Matanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,

Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and

Hayashizaki,Y.

Unpublished (2000)

Contact: Yoshinde Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9212

Fax: 81-45-503-9216

Bmail: genome-ree@gsc.riken.go.jp,

Fax: B1-45-503-9216
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Brail: genome-ree@gac.riken.go.jp,
URI:http://genome.gac.riken.go.jp,
Carninci.p., Nishiyama,Y., Mestover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNR cloning. Methods Enzymol. 303,
ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector MA, and transformed into adaptored by a complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored competent B. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB496626
                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
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/clone_lib="RIXEN full-length enriched, 0 day neonate kidney"
         Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                             84.0%; Score 16.8; DB 10; Length 275; 90.0%; Pred. No. 1.3e+04; rive 0; Mismatches 2; Indels 0;
                                                                                                       /tissue_type="kidney"
/dev_stage="0 day_neonate"
/lab_host="DH108"
                                                          organism≈"Mus musculus"
                                                                    /mol_type="mRMA"
/db_xref="taxon:10090"
                                   Location/Qualifiers
                                                                                              clone="D630004Al2
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                        ORIGIN
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셤

Search completed: July 2, 2004, 13:32:53 Job time : 1500.92 secs

152 Gergekeceeggaagegege 171 1 GGTGCACCGGTGCAGGGGGG 20 Conservative

Local Similarity tes 18; Conserv

Matches

ö

Gaps

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Ö
                                                                                                                                           July 2, 2004, 06:05:50; Search time 134.89 Seconds (without alignments)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                 Run on:
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	566.887 Million cell updates/sec
Title: Develor	US-10-068-160-13
Sequence:	1 tgcaccggtgcaggggggggggggggggggggggggggg
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3373863 segs, 2124099041 residues

6747726 Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seg length: 0 Maximum DB seg length: 200000000

N_Geneseq_29Jan04:*	1: genesegn1980s:*	 3: genesegn2000s:*	4: geneseqn2001as:*	 6: geneseqn2002s:*	 	9: geneseqn2003cs:*	10: deneseon20048:*
Database :							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aac80622 Immunogen	CI	Abl35614 Immunosti	Abl35578 Immunosti	Abl35581 Immunosti	Abl35570 Immunosti	Abl35588 Immunosti	Abk46470 Immunosti	Acc48296 CpG oligo	Acc48300 CpG oligo	Acc48313 CpG oligo	Acc83118 D class C	Acc83152 D class O	Add01049 CpG D oli		Abl35603 Immunosti	Abl35591 Immunosti	Abl35611 Immunosti	Abl35622 Immunosti	Aas09651 Immunorea	Abl35573 Immunosti	Abl35584 Immunosti	Abl35569 Immunosti
SUMMARIES	ŗ	TD	AAC80622	AAS09592	ABL35614	ABL35578	ABL35581	ABL35570	ABL35588	ABK46470	ACC48296	ACC48300	ACC48313	ACC83118	ACC83152	ADD01049	ABL35599	ABL35603	ABL35591	ABL35611	ABL35622	AAS09651	ABL35573	ABL35584	ABL35569
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		rengen	20	20	20	20	20	20	20	20	20	20	20	20	20	20	28	28	28	28	40	20	20	20	20
æ	Query	March	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.1	91.1	91.1	91.1
	300	acore	18	18	18	18	18	18	18	18	13	18	18	18	18	18	18	18	18	18	18	16.4	16.4	16.4	16.4
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Abl35617 Immunosti	Abl35580 Immunosti		Acc48320 CpG oligo	Acc48321 CpG oligo	Acc83125 D class C	Acc83116 D class C	Acc83126 D class C	Add01076 CpG D oli		Abl35590 Immunosti	Abl35594 Immunosti	Abl35606 Immunosti	Abl35602 Immunosti	Aac80602 Imminogen	Aas09572 Immunorea	Abk46450 Immunosti	Abal2385 Human ner	Aal01438 Human rep	Abl96885 Human tes	Aas61882 Porcine m	Aas80037 DNA encod
ABL35617	ABL35580	ACC48311	ACC48320	ACC48321	ACC83125	ACC83116	ACC83126	ADD01076	ADD01059	ABL35590	ABL35594	ABL35606	ABL35602	AAC80602	AAS09572	ABK46450	ABA12385	AAL01438	ABL96885	AAS61882	AAS80037
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16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	c 41	c 42	c 43	0 44	45

### ALIGNMENTS

RESULT 1

AACE	AAC80622
Π	AAC80622 standard; DNA; 20 BP.
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ÄC	AAC80622;
¤	
눔	14-FEB-2001 (first entry)
Ħ	
OE	Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.
ğ	
¥	CpG oligodeoxynucleotide, unmethylated, antiqen-presenting cell;
Ž	immunogenic; cytokine release; natural killer cell; NK cell activation;
Š	cell-mediated immune response; T-cell response; humoral response;
Š	B-cell response, antibody production, immune response induction, vaccine;
Ž	allergy, asthma, infection; bacterial; viral; fungal; protozoal;
3	parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
3	rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
3	immune deficiency; biological warfare agent; cytostatic; antiarthritic;
3	antimicrobial; antiallergic; protozoacide; tuberculostatic;
X	antiasthmatic; dermatological; phosphorothioate; ss.
×	•

12-APR-2000; 2000WO-US009839. 12-APR-1999; 99US-0128898P WO200061151-A2. 19-OCT-2000. Synthetic. 

Ä Verthelyi Klinman D, Ishii K, (KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERT/) VERTHELYI D.

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxymucleotides

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CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5-NAWR-250-AWNN-19. To 5-RY-CpG-RY - 19. The central CpG motif is unmethylated, and the oligonucleotide elivery complex opensising an oligonucleotide of the invention and a targetting to degent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotide of the invention and a targetting and a pharmaceutical composition comprising the oligonucleotide act of alivery complex. The oligonucleotides are able to induce a there a cell-mediated (T-cell) response or a humoral seponse. With coligonucleotides of the sequence 5-NAY-CpG-NAY-3 being able to induce a humoral response. It is thought that after a cell-mediated response and dendritic cells, which then release cyckines, cell-macrophages and dendritic cells, which then release cyckines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then ocut by activation of T- or B-cells. The humoral response can then ocut by activation of T- or B-cells. The chadiorating an allergic reaction (preferably asthma), or an infection, amelocating an allergic reaction (preferably asthma), or an infection, conditions which may be treated include eccema, allergic conditions which may be treated include viral, conditions, and the infections which may be treated include viral, conditions, and the infections which may be treated include viral, conditions, and the infections which may be treated include viral, because the infections which may be treated include viral, conditions, and the infections which may be treated include viral, because the infections which may be treated include viral, conditions, and the infections which may be treated include viral, conditions, and chainstened which may be treated include viral, conditions, and chains and multiple sold allergies and chains and conditions, and conditions which may be treated include viral, cused in the treatment of an autoimmune disorder (e
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Seguence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

.. 100.0%; Score 18; DB 4; Length 20; 100.0%; pred. No. 64; 0; Indels Mismatches ó Query Match
Best Local Similarity 100.0
....hes 18; Conservative

1 TGCACCGGTGCAGGGGGG 18 

ò

RESULT 2 AAS09592 

AAS09592 standard; DNA; 20 BP.

AAS09592;

(first entry) 26-SEP-2001 Immunoreactive CpG sequence-containing oligonucleotide #42.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistcosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic

WO200151500-A1

19-JUL-2001

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ARADUSISTAMBLE TOPICS TO TO TO TO TO TO THE 
                                                                                                                                                                                                                                                                                                                                                 Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of
                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                         Verthelyi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 34; 48pp; English.
                                                                                             14-JAN-2000; 2000US-0176115P.
                               12-JAN-2001; 2001WO-US001122.
                                                                                                                                                                                                                         Ishii K,
                                                                                                                                                                                                                                                                                       WPI; 2001-442129/47
                                                                                                                                                                                                                         Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sedneuces.
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Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

0; Gaps / Match 100.0%; Score 18; DB 4; Length 20; Local Similarity 100.0%; Pred. No. 64; nes 18; Conservative 0; Mismatches 0; Indels Query Match Matches

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1 TGCACCGGTGCAGGGGGG 18 recacceerecaececee 20

à 셤 RESULT 3 ABL35614

ABL35614 standard; DNA; 20 BP. ABL35614; 04-APR-2002 (first entry)

Immunostimulatory oligonucleotide SEQ ID NO: 540.

DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss 

Synthetic.

Location/Qualifiers Key misc RNA

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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, {non-}malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allargies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
/*tag= a
/note= "optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                    New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
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/note= "optionally thymidine is replaced by uracil to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 6; Length 20; 100.0%; Pred. No. 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 62; 68pp; English.
                                                                                                                                                                                                                                                                      Klinman DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TGCACCGGTGCAGGGGGG 18
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                                                                                                                                                             07-JUN-2001; 2001WO-US018276.
                                                                                                                                                                                                 07-JUN-2000; 2000US-0209797P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL35578 standard; DNA; 20
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nes 18; Conservative
                                                                                                                                                                                                                                    (BIOS-) BIOSYNEXUS INC.
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                                                                                                                                                                                                                                                                    Flora M,
                                                                                        WO200193902-A2
                                                                                                                          13-DEC-2001
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                                                                                                                                                                                                                                                                      Mond JJ,
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Matches
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comprises at least one oligonate comprising both an RNA region and a DNA region. The composition is useful for character adjuvant and in treating cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, overy, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or altergies (e.g. altergic rhinitis, hay fever or food altergies), Lyme diseases, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                          new immunostimulatory compositions comprising RNA/DNA hybrid oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersemaitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulatory oligonucleotide SEQ ID NO: 507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 18; 100.0%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 61; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                      Klinman DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCACCGGTGCAGGGGG 18
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                                                                                                                     07-JUN-2001; 2001WO-US018276.
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Best Local Similarity luv...
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                                                                                                                                                                                     (BIOS-) BIOSYNEXUS INC.
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                                                                                                                                                                                                                      Flora M,
                                                    WO200193902-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
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                                                                                  13-DEC-2001
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                                                                                                                                                                                                                      Mond JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc RNA
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ID ABL
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Gaps ..

0; Indels

Mismatches

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BP.

New immunostimulatory compositions comprising RNA/DNA hybrid oligomuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

Mond JJ, Plora M, Klinman DM

WPI; 2002-130570/17.

(BIOS-) BIOSYNEXUS INC

07-JUN-2001; 2001WO-US018276. 07-JUN-2000; 2000US-0209797P.

13-DEC-2001.

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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytoxines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant treating diseases, including pathogenic infection, non-)malignant colon, or cancers of the brain, lung, ovary, breast, prostate or colon, or carcinoma and sarcomas), autoimmune diseases or allergies (e.g. allergic thinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunosimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..20
/*tag= a
/note= "optionally thymidine is replaced by uracil to
/note= "optionally hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA/RNA hybrid; phosphorothicate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bic-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                               oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                          compositions comprising RNA/DNA hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 6; Length 20; 100.0%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             Example 11; Page 61; 68pp; English.
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                                                                                                                                                                                        Klinman DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGCACCGGTGCAGGGGGG 18
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                                                                                07-JUN-2001; 2001WO-US018276.
                                                                                                                  07-JUN-2000; 2000US-0209797P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                     (BIOS-) BIOSYNEXUS INC.
                                                                                                                                                                                                                                                          New immunostimulatory
                                                                                                                                                                                                                         WPI; 2002-130570/17.
                                                                                                                                                                                        Flora M,
                WO200193902-A2
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                                                                                                                                                                                        Mond JJ,
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The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytckines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant trumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a //*tag= a //*tag= hymidine is replaced by uracil to //ncte= "optionally thymidine is linked to at least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 64; Matches 18; Conservative 0; Mismatches
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misc_RNA
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ID ABL3
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us-10-068-160-13.rng

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WPI; 2002-227118/28
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                                                                                                                                                                                                                                                      The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, {non-}malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or cancers and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, preventing, HIV or malaria. The composition is also useful for treating, preventing or amaliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of
                                                                                                                                                         New immunostimulatory compositions comprising RNA/DNA hybrid oligomuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory unmethylated CpG oligodideoxynucleotide #60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                               Example 11; Page 61; 68pp; English.
                                                                                                 Klinman DM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCACCGGTGCAGGGGG 18
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             07-JUN-2001; 2001WO-US018276.
                                          07-JUN-2000; 2000US-0209797P
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                                                                    (BIOS-) BIOSYNEXUS INC.
                                                                                                                            WPI; 2002-130570/17
                                                                                                 Flora M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention
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                                                                                                 Mond JJ,
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Matches
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ABK46470
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(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

10-AUG-2000; 2000US-0224011P.

Klinman DM

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Prince

Mond JJ,

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                                                                                                                 The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligoddeoxymucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have ronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxymucleotide that can be used in the creation of the vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CpG oligodeoxymucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae P protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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for activating the immune system to treat diseases such as cancer,
comprises contacting a dendritic cell precursor with a D type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CpG oligodeoxymucleotide D29 used for dendritic cell maturation.
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/mod_base= OTHER
/note= "OTHBR= phosphorothioate nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 18; DB 6; Length 20; 100.0%; Pred. No. 64; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGCACCGGTGCAGGGGG 20
                                                                                    Claim 4; Page 8; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGCACCGGTGCAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
Hes 18; Conservative
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modified_base
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Gaps

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The present sequence is that of a CpG oligodeoxynucleotide of the invention. A claimed method for generating dendritic cells involves contacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxynucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature dendritic cells and enhancing Tell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
cell precursor, such as a monocyte, with such an oligodeoxymucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antiqen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune
                                                                      response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating mature dendritic cells for tumor immunotherapy or as vacor activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.
                                                                                                                                                                                              .Match
Local Similarity 100.0%; Pred. No. 64;
ies 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                             Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 61; 69pp; English.
                                                                                                                                                                                                                                                                          1 TGCACCGGTGCAGGGGG 18
                                                                                                                                                                                                                                                                                                3 TGCACCGGTGCAGGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                       ACC48313 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CpG oligodeoxynucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
                                                                                           cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generating mature dendritic cells for tumor immunotherapy or as vaccines
                                                                      The present sequence is that of D type CpG oligodeoxynucleotide D29, which is used in a claimed method for generating a mature dendritic cell. The method involves contacting a dendritic cell precursor, especially a monocyte, with the oligonucleotide. The method is useful for generating mature dendritic cells and enhanning T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated T lymphocytes
                                                                                                                                                                                                                                                                                                                                                  Gaps
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/note= "N is any base {especially G} or
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                                                                                                                                                                                                                                                                            Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                     Claim 11; Page 44; 69pp; English.
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/note= "N is
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-2003 (first entry)
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   oligodeoxynucleotide
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ACC83118 standard; DNA; 20 BP. RESULT 12 ACC83118

ACC83118;

(first entry) 27-AUG-2003

D class CpG ODN sequence useful for encapsulating in SSCL, DV29.

Sterically stabilised cationic liposome, SSCL, ODN, oligodeoxynucleotide, tuberculosis, cytokine; leishmanisais, AlDS-associated Kaposi's tumour; thyroid, cancer; allergy, eczema; allergic rhinitis, coryza, hay fever; schistosomiasis, interferon gamma; uluus erythematosus, antimicrobial; sthistosomiasis, interferon gamma; lupus erythematosus, antimicrobial; cytograma; last man, tricaria; autoimmum disease; diabetes; rheumatoid arthritis; cyG motif: interleukin-13; cytostatic; tularemia; malaria; psoriasis; autiliple sclerosis, infection; tumour; ss.

Unidentified

WO2003040308-A2,

15-MAY-2003

29-JUL-2002; 2002WO-US024235

27-JUL-2001; 2001US-0308283P. 25-JUL-2002; 2002US-00206407.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK; Klinman DM,

WPI; 2003-482260/45.

Cationic liposome composition for delivering oligodeoxymucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.

Disclosure; Fig 10C; 110pp; English

The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a collipid, stabilising agent and encapsulating a K type oligodeoxymuclectide (ODN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing control in the invention is useful in pharmaceutical composition for impairing a control in a subject; for stimulating an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an in vivo or immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxymucleotides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, applications; for treating infectious and leishmaniasis), cancer (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer (e.g. solid tumours, allergic asthma, urticaria, food allergies), autoimmune diseases (e.g. diabetes, theumatodia arthritis, lupus erythematosus and formulating selerosis) and postiasis. The present sequence is a D class CpG on the control of the con ODN potentially useful for encapsulating in SSCL 

Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

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100.0%; Score 18; DB 8; Length 20; ilarity 100.0%; Pred. No. 64; Conservative 0; Mismatches 0; Indels
 Query Match
Best Local Similarity
Matches 18; Conservat
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Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide; tuberculodis; grotkine; leishmaniasis; AlDS-associated Kaposi's tumour; thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever; schistosoxiasis; interferon gamma; lupus erythematosus; antimicrobial; asthma; urticaria; autoimmune disease; diabetes; rheumatodi arbhritis; CpG motif; interfeutin-13; cytostatic; tularema; malaria; psoriasis; multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
                                                                                                   D class ODN sequence useful for encapsulating in SSCL,
 18
           20
         3 TGCACCGGTGCAGGGGGG
                                                     ACC83152 standard; DNA; 20
                                                                                   27-AUG-2003 (first entry)
                                                                     ACC83152;
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                                      RESULT 13
                                               ACC83152
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(USSH ) US DEPT HEALTH & HUMAN SERVICES 27-JUL-2001; 2001US-0308283P. 25-JUL-2002; 2002US-00206407. Klinman DM, Gursel I,

29-JUL-2002; 2002WO-US024235.

WO2003040308-A2

15-MAY-2003.

Location/Qualifiers
16. .20
4.tag= a
/mod base= OTHER
/note= "Phosphorothioate backbone"

Key modified\_base Unidentified

Puri RK; Ishii KJ, Kawakami K, Joshi BH,

WPI; 2003-482260/45.

Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.

Example 8; Page 52; 110pp; English.

The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilising agent and encapsulating a K type oligodeoxymucleotide (ODN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing a CpG motif. The invention is useful in pharmaceutical composition for impairing an immune relation in a subject; for stimulating an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an in vivo or an invitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxymucleotides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, capplications; for treating infectious diseases (e.g. tularemia, malaria, capplications; allergic asthma, unticaria, food allergies), cancer cells. allergic asthma, unticaria, food allergies), autoimmune diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and multiple solerosis) and psoriasis. The present sequence is a D class odn potentially useful for encapsulating in SSCL

G; 2 T; 0 U; 0 Other; BP; 2 A; 4 C; 12 20 Sequence ø

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Score 18; DB 8;
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RESULT 14

ADD01049 standard; DNA; 20 ADD01049 

ADD01049;

01-JAN-2004 (first entry)

CpG D oligonucleotide SEQ ID NO:13.

vascular endothelial growth factor; VEGF; CpG oligonucleotide; neovascularisation; angiogenesis; vulnerary; vasotropic; antiarteriosclerotic; gene therapy; skin graft; male pattern baldness; atherosclerosis; ischaemia; ss.

Synthetic

WO2003054161-A2.

03-JUL-2003

19-DEC-2002; 2002WO-US040955

20-DEC-2001; 2001US-0343457P.

(UYTE-) UNIV TENNESSEE RES CORP. (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Klinman DM, Zheng M, Rouse BT;

4PI; 2003-559138/52.

Inducing the production of vascular endothelial growth factor by a cell, useful for inducing angiogenesis, comprises contacting the cell with a CpG oligodeoxynucleotide.

Example 7; SEQ ID NO 13; 37pp; English.

The present invention describes a method for inducing the production of vascular endothelial growth factor (VEGF) by a cell comprising contacting the call with a CpG oligonuclectide and therefore inducing the production of VEGF by the cell. Also described: [1] inducing neovascularisation in a tissue, comprising introducing a CpG oligonuclectide into an area of the cilisue where the formation of new blood vessels is desired, and so inducing neovascularisation in the area of the tissue, [2] promoting angiogenesis in an area of the subject where angiogenesis is desired, comprising introducing a CpG oligonuclectide to the area, and so promoting angiogenesis in the subject; and [3] screening for an agent that inhibits neovascularisation, comprising administering a CpG oligonuclectide to a non-human mammal and administering a CpG oligonuclectide to a non-human mammal and administering a CpG oligonuclectides have vulnerary, vasctropic and antiarteriosclerotic coligonuclectides can be used in gene therapy. The method and the CpG oligonuclectides can be used in gene therapy. The method and the CpG oligonuclectides can be used in new pagiogenesis or cathorities, and can be used in new pagiogenesis or an extension, such as in subjects with a skin graft, subjects who exhibit male pattern baldness, or subjects who have a wound or who have atherosclerosis or ischaemia. The method may also be used in screening cor exhibit male pattern belong may also be used in screening cor processed in the exemplification of the processed in the exemplification of the processed in the covasculariation. The present sequence the present invention

Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                 DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
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Query Match
100.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                   Immunostimulatory oligonucleotide SEQ ID NO: 525.
                               1 TGCACCGGTGCAGGGGG 18
                                        3 TGCACCGGTGCAGGGGG 20
                                                                                      ABL35599 standard; DNA; 28
                                                                                                                     04-APR-2002 (first entry)
                                                                                                     ABL35599;
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ABL35599
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1. .28 //t.ds a //t.d WO200193902-A2 13-DEC-2001.

Location/Qualifiers

Synthetic. Key misc\_RNA 07-JUN-2001; 2001WO-US018276. 07-JUN-2000; 2000US-0209797P.

(BIOS-) BIOSYNEXUS INC

Mond JJ, Flora M, Klinman DM;

WPI; 2002-130570/17.

New immunostimulatory compositions comprising RNA/DNA hybrid oligonuclectides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

Example 11; Page 61; 68pp; English.

The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic thinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a biowarfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of

Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match

100.0%; Score 18; DB 6; Length 28;

0; Gaps Best Local Similarity 100.0%; Pred. No. 63; Matches 18; Conservative 0; Mismatches 0; Indels

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Search completed: July 2, 2004, 08:31:33 Job time : 135.89 secs Б

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2	<ol> <li>2004, 07:36:05; Search time 633.732 Sec (without alignments)</li> <li>1231.080 Million cell</li> </ol>	Seconds } 11 updates/sec
Title: US-10-0 Perfect score: 18 Sequence: 1 tgcac	US-10-068-160-13 18 1 tgcaccggtgcagggggg 18	
Scoring table: IDENTITY NUC Gapop 10.0,	TY NUC 10.0 , Gapext 1.0	
Searched: 3470272	seqs, 21671516995 residues	
Total number of hits sa	satisfying chosen parameters: 6940544	
Minimum DB seq length: Maximum DB seq length:	2000000000	
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 507 13-DEC-2001,
Biosynexus Incorporated (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 514 13-DEC-2001;
Biosynexus Incorporated (US)
     Pred. No. 4.2e+02;
; Mismatches 0;
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                                                     1 TGCACCGGTGCAGGGGG 18
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Patent: WO 0193902-A 496 13-DEC-2001;
Biosynexus Incorporated (US)
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Patent: WO 0193902-A 504 13-DEC-2001;
Biosynexus Incorporated (US)
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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Patent: WO 0193902-A 525 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 529 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
                            Mond,J.J., Flora,M. and Klinman,D.M.
Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 517 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                    100.0%; Score 18; DB 6; L ilarity 100.0%; Pred. No. 4.1e+02; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/wol_type="unassigned DNA"
/db_xref="texon:32630"
/noTe="Synthetic HDR"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

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    /organism="synthetic construct"

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Sequence 525 from Patent WO0193902.
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Vaccine against RSV
Patent: Wo 0211761-A 60 14-FEB-2002;
HENRY W. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Location/Qualifiers
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/mol type="unassigned DNA"
/morstef="taxon:32630"
/note="Synthetic oligonucleotide"
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100.0%; Pred. No. 4.2e+02;
iive 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Synthetic HDR"
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           Sequence 540 from Patent W00193902.
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Sequence 517 from Patent WO0193902.
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Sequence 60 from Patent W00211761.
AX465392
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AX352221.1 GI:18617504
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Klenk, H. P., Clayton, R. A., Tomb, J.-F., White, O., Nelson, K. E.,
Kenk, H. P., Clayton, R. A., Tomb, J.-F., White, O., Nelson, K. E.,
Ketchum, K. A., Dodson, R. J., Gwinn, M., Hickey, E. K., Peterson, J. D.,
Richardson, D. L., Kerlavage, A. R., Graham, D. E., Kyrpides, N. C.,
Kirkness, E. K., Dougherty, B. A., McKenney, K., Adams, M. D., Loffus, B.,
Krikness, E. F., Dougherty, B. A., McKenney, K., Adams, M. D., Loffus, B.,
Peterson, S., Reich, C. I., McNeil, L. K., Badams, M. D., Loffus, B.,
Thou, L., Overbeek, R., Gocayne, J. D., Weidman, J. F., McDonald, L.,
Utterback, T., Cotton, M. D., Spriggs, T., Artiach, P., Kaine, B. P.,
Sykes, S. M., Sadow, P. W., D'Andrea, K. P., Bowman, C., Fujii, C.,
Garland, S. A., Mason, T. M., Olsen, G. J., Frseer, C. M., Smith, H. O.,
Woese, C. R. and Venter, J. C.
Direct Submission
Submission
Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
K. In order to show the genes in ascending order on the genome, the
original version has been moved by TIGR to position 2093570
of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus DSM 4304
Archaeoglobus fulgidus DSM 4304
Archaeoglobus tilgidus DSM 4304
Archaeoglobus tilgidus DSM 4304
Archaeoglobaceae, Archaeoglobi; Archaeoglobales;
Archaeoglobaceae, Archaeoglobus,
Srienk,H.P., Clayton,R.A., Tomb,J., White,O., Nelson,K.E.,
Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C.,
Richardson,D.L., Rerlavage,A.R., Graham,D.E., Kyrpides,N.C.,
Rixhness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.P., McDonald,L.,
Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Rowman,C., Fujii,C.,
Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
Woese,C.R. and Venter,J.C.
The complete genome sequence of the hyperthermophilic,
sulphate-reducing archaeon Archaeoglobus fulgidus
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vvefhylyptekrygllllsyiwagneaitpcepsswrdlyevspngagtskfyyekl
pesgnitlkissgkeegkylfpfalggattitatasgapatshgydlatoinsavysl
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Archaecglobus fulgidus DSM 4304 section 105 of 172 of the complete
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/product="A. fullgidus predicted coding region AF1454"
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/gene="AF1454"
/note="hypothetical protein; identified by GeneMark;
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Location/Qualifiers
1. 10782
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complement(195)
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  1 TGCACCGGTGCAGGGGG 18
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AE001002.1 GI:2689325
                               16 TGCACCGGTGCAGGGGG
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                                                                                                                  Query Match
100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 537 13-DEC-2001;
Blosynexus Incorporated (US)
Location/Qualifiers
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Patent: WO 0193902-A 548 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
/note="Synthetic HDR"
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/mol type="unassigned DNA"
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/note="Synthetic HDR"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
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Sequence 548 from Patent WO0193902.
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Sequence 537 from Patent WO0193902.
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synthetic construct
artificial sequences.
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORGANISM
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Matches
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VERSION
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AUTHORS
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AX352252
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LOCUS
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SIGDYVLPERFOIKVIVDSRELRSBVWKHLREIGAKIEIRNLEVADYVVSDRVAVERK
TVEDPLINSIIQKERLPSQVARLKSAYSRPVIIIBGENPYRGCYHPNAVRGAIASLIID
FGIPVLRSSNARETALIFAMARROSERKRCVVEHTAKTKRTLKDEDRYIVSAISNY
GNVIARNILLDYPÇTIENIATADEBEELAKVPKVGKKIAKRIRRVMTTPYSGRAGFYDSES
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SILABINKACQHAVELI ETQSYRAVKSYIRKUNREATSKGSSKAAKSI VEDDI PKKKAVI
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GQASRDNDKGMRQKEQI ETI DKFRRGVYKVLVATSVGEEGLDI PSTDLVVFYBAVPSE
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[219. .5444
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transl_table=
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AIFVNYSHFRHESRSKRAYPLYILLFVFWLLNISLTFRFLPLEFRFAIYTLSVAVILI
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                                                                                                                                                                                                                                                                                                               complement(560s. .5817)
complement(560s. .5817)
forene=n8741459"
foreign to GB:L77117 SP:O57735 PID:1499069 percent identity: 35.38; identified by sequence similarity;
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; Pred. No. 6.5e+02;
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complement (5605. .5877)
5471. .5543
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6658. .689
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Best Local Similarity
Matches 17; Conserv
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RESULT 14 AX194501

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AX194501 AX194501.1 GI:15385157
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                                                                                                                                           Klinman, D., Ishii, K. and Verthelyi, D.
Oligodeoxymuclectide and its use to induce an immune response patent: WO 0151500-A 101 19-JUL-2001;
Secretary of the Department of Health and Human Services (US) Location/Qualifiers
1. 20
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91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 495 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="Synthetic HDR"
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Sequence 495 from Patent W00193902.
AX352199.1 GI:18617482
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AUTHORS
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Search completed: July 2, 2004, 10:07:58 Job time : 636.732 secs

Sequence Sequence Sequence Sequence Sequence

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OM nucleic

Run on:

Sequence:

Searched:

us-10-068-160-13.rni

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Sequence 20, Appl
Sequence 77, Appl
Sequence 178, App
Sequence 2752, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 7532, Ap
Sequence 7632, Ap
Sequence 7632, Ap
Sequence 7831, Ap
Sequence 3, Appli
Sequence 7949, Ap
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Patent No. 6046711
GENERAL INFORMATION:
APPLICANT: HINUMA, SHUJI
APPLICANT: FUKUSUMI, SHOJI
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 3; Length 1443; Pred. No. 2.4e+02; 0; Mismatches 2; Indels 0
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US-09-13-381-178
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US-09-511-881A-2
US-09-511-881A-2
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US-09-171-18-3
US-08-031-148-3
US-09-205-991A-7949
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MEDIUM TYPE: Disketer
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketer
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASSISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,38LA
FILING DATE: 28-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 286823/1996
FILING DATE: 29-OCT-1996
FILING DATE: 20-OCT-1996
FILING DATE: 20-OCT-1996
FILING DATE: 20-OCT-1996
FILING DATE: 30-OCT-1996
FILING DATE: 30-OCT-1997

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Best Local Similarity 88.9%;
Matches 16; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-959-381A-3/c
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                                                                                                                                                                                                                                         July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
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354.132 Million cell updates/sec
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-170-496D-81

US-09-170-496D-207

US-08-959-381A-4

US-09-248-171-2

US-09-740-027-3

US-09-740-027-3

US-09-740-027-3

US-09-22-991A-385

US-09-22-991A-385

US-09-22-991A-386

US-09-25-991A-386

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US-08-441-591-19
US-08-303-362A-18
US-08-303-362A-19
PCT-US95-05600-35
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Result 2

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Gaps

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US-09-248-571-2

1 Sequence 2, Application US/09248571

1 Sequence 2, Application US/09248571

2 GENERAL INPORMATION:

APPLICANT: BASBAUM, CAROL

APPLICANT: GENERALORS, MARIANNE

APPLICANT: GENERALORS, LASERA

APPLICANT: GENERALORS, LASERA

APPLICANT: GENERALORS COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN

TITLE OF INVENTION: GENE EXPRESSION

TITLE OF INVENTION: GENE EXPRESSION

FILE REFERENCE: UCSP12/02

CURRENT APPLICATION NUMBER: US/09/248,571

CURRENT APPLICATION NUMBER: 60/074,398

EARLIER PILING DATE: 1998-02-11

SEQ ID NO 2

SEQ ID NO 2

TYPE: NANA

TYPE: NANA

TYPE: NANA

TYPE: NANA

TYPE: NANA
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TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR ITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR ITLE OF INVENTION: POLYNUCLEOTIDES NUMBER OF SEQUENCES: SORRESPONDENCE ADDRESS: ADDRESSER: Ratner & Prestia STREET: P.O. Box 980 CITY: Valley Forge STATE: PA COUNTRY: USA 21P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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MEDIUM TYPE: Diskette COMPUTER. IEM COMPATIBLE COMPUTER. IEM COMPATIBLE COMPUTER. IEM COMPATIBLE COMPUTER. IEM COMPATIBLE CONFURER. FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/959,381A FILING DATE: 28-CCT-1997
CLASSIFICATION: DATA: 286823/1996
APPLICATION NUMBER: 29,031
PREJENCAPION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: TAK-50003
TELECHONE: 610-407-0700
TELERAX: 610-407-0700
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
US-09-248-571-2
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MOLECULE TYPE:
US-08-959-381A-4
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10.496D-81/C
15.69quence 81, Application US/09170496D
15.69quence 81, Application US/09170496D
15.6quence 81, Application US/09170496D
15.6quence 81, Application US/09170496D
15.6TECANT: Behan, Dominic P.
15.6APPLICANT: Behan, Dominic P.
16.6APPLICANT: Diaw, Chen W.
17.1TLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
17.1TLE OF INVENTION: Receptors
17.1TLE OF INVENTION: Receptors
17.1TLE OF INVENTION: Receptors
17.1TLE OF INVENTION: Receptors
17.1TLE OF INVENTION: 10.655339-Endogenous, Constitutively Activated Human G Protein-
17.1TLE OF INVENTION: 10.655339-Endogenous, Constitutively Activated Human G Protein-
17.1TLE OF INVENTION: 10.969-10-13
17.1TLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-170-496D-207/c
10S-09-170-496D-207/, Application US/09170496D
10S-09-170-496D-207, Application US/09170496D
10S REAL INFORMATION:
10S PAPLICANT: Behan, Dominic P.
10S APPLICANT: Chalmers, Derek T.
10S APPLICANT: Liaw, Chen W.
10S TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-1TILE OF INVENTION: Receptors
1 FILE REFERENCE: AREN-0040
1 CURRENT PILING DATE: 1998-10-13
1 NUMBER OF SEQ ID NOS: 294
1 SOFTWARE: Patentin version 3.1
1 SEQ ID NO 207
1 LENGTH: 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 4;
Pred. No. 2.4e+02;
0; Mismatches 2;
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US-08-959-381A-4/c
; Sequence 4, Application US/08959381A
; Satent No. 6048711
; GENERAL INFORMATION:
; APPLICANT: HINUMA, SHUJI
; APPLICANT: FUKUSUMI, SHOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCACCGGTGCAGGGGG 18
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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CORGANISM: Homo sapiens
US-09-170-496D-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
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RESULT 7
US-09-740-027-3

Sequence 3, Application US/09740027

Sequence 3, Application US/09740027

Patent No. 6485939

GENERAL INFORMATION:
PAPPLICANT: NA. Jane et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: OCA-CTOR PROTEINS, MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
TITLE OF INVENTION: OCA-CTOR PROTEINS, AND USES THEREOF
TILE REPERRANCE: CLOO1052

CURRENT APPLICATION NUMBER: US/09/740,027

CURRENT APPLICATION NUMBER: US/09/740,027

SOFTWARE: Patence of Windows Version 4.0

SOFTWARE: Patence of Windows Version 4.0

SOFTWARE: Patence of Windows Version 4.0
                                                                                                                                                                                                                                                                 RESULT 6

19-09-53-736-2

1 Sequence 2, Application US/09553736

2 Patent No. 6440672

2 GENERAL INFORMATION:

3 APPLICANT: BASBAUM, Carol

3 APPLICANT: BASBAUM, Carol

4 APPLICANT: GENERALION: Marianne

5 APPLICANT: GENERALION: Marianne

5 APPLICANT: GENERALIONEL, Assefa

APPLICANT: GENERALIONEL, Assefa

5 TITLE OF INVENTION: MUCIN GENE EXPRESSION

5 FILE REFERENCE: USF 012/03US

6 CURRENT APPLICATION NUMBER: USF 04-20

7 PRIOR FILING DATE: 1999-02-11

7 PRIOR PLING DATE: 1999-02-11

7 PRIOR PLING DATE: 1999-02-11

7 SEQ ID NO 2

7 SEQ ID NO 2

7 LENGTH: 3358
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Query Match 82.2%; Score 14.8; DB 3; Length 3358; Best Local Similarity 88.9%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

82.2%; Score 14.8; DB 4; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0
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Best Local Similarity 88.9
Matches 16; Conservative
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CORGANISM: Homo sapiens
US-09-553-736-2
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; ORGANISM: Human
US-09-740-027-3
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Sequence 1, Application US/09922445 Patent No. 6528268 GENERAL INFORMATION:

RSULT 8 JS-09-922-445-1/c

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RESULT 10
US-09-023-655-668
US-09-023-655-668
; Sequence 668, Application US/09023655
; Patent No. 6607879
; Patent No. 6607879
; APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stutant
; APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
APPLICANT: PALOALTO
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/nn --
FILLN: nnmm
                                                    Query Match 80.0%; Score 14.4; DB 4; Best Local Similarity 93.8%; Pred. No. 3.7e+02; Matches 15; Conservative 0; Mismatches 1;
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CLASSIFICATION:
ATTORNEY/GREAT INFORMATION:
NAMB: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 668:
SEQUENCE CHARACTERISTICS:
FENGTH: 2194 base pairs
or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-252-991A-736
; Sequence 736, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
; OTHER INFORMATION: a, t, c, g, US-09-313-294A-385
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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APPLICATION NUMBER:
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LIBRARY: EOSI
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                                                                   OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be OTHER INFORMATION: A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNULBOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.2%; Score 14.8; DB 4; Length 38653; Best Local Similarity 88.9%; Pred. No. 2.3e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;
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OTHER INFORMATION: Incyte ID No. 6476212 700549120H1
NAME/KEY: unsure
LOCATION: 3, 7, 39, 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
| LOCATION: (36405)...(36523)
| OTHER INFORMATION: |
| NAME/KEY: LILLON: (36524)...(38341)
| OTHER INFORMATION: |
| OTHER INFORMATION: |
| NAME/KEY: exon
| LOCATION: (38342)...(38653)
| LOCATION: (38342)...(38653)
| OTHER INFORMATION: |
| DUBLICATION INFORMATION: |
| DATABASE ACCESSION NUMBER: Genbank/AC004923 |
| DATABASE ENTRY DATE: 1999-12-21 |
| NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-313-294A-385; Sequence 385, Application US/09313294A; Parent No. 6476212; General No. 6476212; APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14712 recacresecadeses 14695
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                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: (34315)..(34588)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (34589)..(36404)
OTHER INFORMATION:
              ..(32163)
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LENGTH: 265
TYPE: DNA
ORGANISM: Zea mays
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Sequence 4, Application US/08809523

Sequence 4, Application US/08809523

Patent No. 6207416

GENERAL INFORMATION:

APPLICANT: Sarev, Sergei. A., Emerson,

APPLICANT: Suzamne U., Purcell, Robert H.

TITLE OF INVENTION: Recombinant Proteins Of Hepatitis E And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines

NUMBER OF SEQUENCES: 107

CORRESPONDENCES: 107

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA
                                                                                                ZIP: 10154
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPRERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,316
FILING DATE: 11-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124459
FILING DATE: CLASSIFICATION: 36,459
REPERENCE/DOCKET WUMBER: 2026-4255
REFERENCE/DOCKET WUMBER: 36,459
REFERENCE/DOCKET WUMBER: 2026-4255
TELECOMMUNICATION INFORMATION:
TELESTRAK: (212) 758-4800
TELESTRAK: (212) 751-6849
INPORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7168 base paire
TWORP: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOBY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1995
FILING DATE: US/08/316,765
FILING DATE: US/08/316,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2263 CCGGTGCAGGGGG 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-840-316-4
                 NEW YORK
NEW YORK
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-809-523-4/c
                                                                      COUNTRY:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANTY: Marc J. Rubenfield et al.
TITLE OF INVENTION: AZEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 736
IENGTH: 732
TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-736
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US-09-252-991A-677/c

US-09-252-991A-677/c

Squence 677, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:

APPLICATION:

TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 677

LENGTH: 1350

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-677
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APPLICANT: Emeraton, Suzanne U., Purcell, Robert H.,
APPLICANT: Emeraton, Suzanne U., Purcell, Robert H.,
APPLICANT: Tarrev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of Hepatitis E And Their
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Dee In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.8%; Score 14; DB 4; Length 732
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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US-08-840-316-4/c
US-08-840-316-4/c
Sequence 4, Application US/08840316
Patent No. 6054567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 GCACCGGTGCAGGG 536
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     Length 7168;
Query Match 77.8%; Score 14; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0;
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Query Match 77.8%; Score 14; DB 3; Length 7168; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              Search completed: July 2, 2004, 13:37:23 Job time: 29.2073 secs
                                                                                                                          2263 CCGGTGCAGGGGG 2250
                                                                                                          5 CCGGTGCAGGGGGG 18
                       ; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-971-4
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                                                                                                                                                                                                                    Length 7168;
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                  Query Match 77.8%; Score 14; DB 3; Le Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 14; Conservative 0; Mismatches 0;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/947,263

FILING DATE: 18-58P-1992

ATTORNEY ACENT INFORMATION:
NAME: RICHART W. BORK
REGISTRATION NUMBER: 2026-4(
TELECASTRATION NUMBER: 2026-4(
TELEPANCE) DOCKET NUMBER: 2026-4(
TELEPANCE) TOSA-4800
TELEPANCE: (212) 759-4800
TELEPANCE (212) 751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-809-523-4
                                                                                                                                                                                                                                                                           2263 CCGGTGCAGGGGGG 2250
                                                                                                                                                                                                                                                             5 CCGGTGCAGGGGG 18
                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-471-971-4/c
                                                                                                                                                                                                                                                             Š
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## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds

(without alignments)
625.926 Million cell updates/sec
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Title:
Perfect score: 18
Sequence: 18
Scoring table: IDENTITY NUC
Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : Published Applic

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Published Applications NA: "

(cgn2 6/ptodate/2/pubpna/USO7 PUBCOMB.seq: "

(cgn2 6/ptodata/2/pubpna/USO7 NEW PUB.seq: "

(cgn2 6/ptodata/2/pubpna/USO6\_NEW PUB.seq: "

(cgn2 6/ptodata/2/pubpna/USO6\_NEW PUB.seq: "

(cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq: "

(cgn2 6/ptodata/2/pubpna/USO9 NEW PUB.seq: "

(cgn2 6/ptodata/2/pubpna/USO0 PUBCOMB.seq: "

(cgn2 6/ptodata/2/pubpna/USO0 PUBCOMB.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		App1		App	App.	App ,	App.	Appli	42, Appl	2, Appli		App	Ξ.	~	App.
	_	13,	496	504	507	514,	540	7	42,	2,	178,	517	525,	529	537
	Description	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	ΩI	US-10-068-160-13	US-09-874-991C-496	US-09-874-991C-504	US-09-874-991C-507	US-09-874-991C-514	US-09-874-991C-540	US-10-068-160-2	US-10-194-035-42	US-10-666-022-2	US-10-666-022-178	US-09-874-991C-517	US-09-874-991C-525	US-09-874-991C-529	US-09-874-991C-537
		15	13	13	13	13	13	15	15	17	17	13	13	13	13
	Query Match Length DB	18	20	20	20	20	20	20	20	20	20	28	. 28	28	. 58
ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	18	18	18	18	18	13	18	18	18	18	18	18	18	18
	Result No.		7	m	4	IJ	9	7	ω	o,	10	11	12	13	14

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Sequence Seq	Sequence
US-09-874-991C-548 US-09-874-991C-548 US-09-874-991C-499 US-09-874-991C-549 US-09-874-991C-506 US-09-874-991C-510 US-10-68-160-58 US-10-194-091C-510 US-10-194-091C-510 US-09-874-991C-516 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-09-874-991C-528 US-10-10-194-091C-528 US-10-194-091C-528 US-10-194-091C-528 US-10-194-091C-528 US-10-194-091C-528 US-10-194-091C-528 US-10-027-632-68267 US-10-027-632-68267 US-10-027-632-68267 US-10-027-632-108181 US-10-027-632-143906	-10-027-632-14390
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#### ALIGNMENTS

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Sequence 11, Application US/10068160;
Sequence 11, Application NG 1020030060440A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE STAPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SERVICANT: SERVICES
APPLICANT: STAIL Ken
APPLICANT: STAIL Ken
TILLS OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REPRESENTE: 2002-02-06
FILE REPRESENTE: 2002-02-06
FILE REPRESENTE: 2002-02-06
FILE REPRESENTE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PAREMIT NOS: 120
SOFTWARE: PAREMIT NOS: 120
SOFTWARE: PAREMIT NOS: 130
TYPE: DAM
TYPE: DA
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1 TGCACCGGTGCAGGGGG 18

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-514
                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-99IC-507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-874-991C-514
US-09-874-991C-514
Sequence 514, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND. JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KINNAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT APPLICATION NUMBER: 60/209,797
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 514
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18; DB 13; Length 20; llarity 100.0%; Pred. No. 42; Conservative 0; Mismatches 0; Indels
          CURRENT APPLICATION NUMBER: US/09/874,991C CURRENT FILING DATE: 2001-06-07 PRIOR APPLICATION NUMBER: 60/209,797 PRIOR FILING DATE: 2000-06-07 NUMBER OF SEQ ID NOS: 620 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGCACCGGTGCAGGGGG 18
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FILE REFERENCE: 07787.0042-0
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Best Local Similarity 100.0
Matches 18, Conservative
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Matches 18; Conserv
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 504, Application US/09874991C

Publication No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: TLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 7078 1042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT PILING DATE: 2001-06-07
PRIOR FILLING DATE: 2000-06-07
PRIOR FILLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SEQ ID NO 504
LENGTH: 20
                                                                      APPLICANT: MOND, JAMES J.
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: KILNMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
CURRENT APPLICATION NUMBER: 0.677
CURRENT PILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 496
LENGTH: 20
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Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: KLINAN, MICHAEL
APPLICANT: KLINAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels
     Application US/09874991C
.. US20040052763A1
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                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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US-09-874-991C-507
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Gaps

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Publication No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOUND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNES M.
ITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR PLING DATE: 2000-06-07
PRIOR PLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
                                                      ö
100.0%; Score 18; DB 13; Length 20; 100.0%; Pred. No. 42; tive 0; Mismatches 0; Indels
                                                                                                           1 TGCACCGGTGCAGGGGG 18
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; SEQ ID NO 540
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRATIRE:
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18-10-006-100-13. INDD

US-10-068-160-2

Sequence 2, Application US/10068160

Publication No. US20030060440A1

GENERAL INFORMATION:

APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: VERTHELYI, Daniela

TITLE OF INVERTYON: OLIGODEXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

FILE REFERENCE: 4239-6199

CURRENT APPLICATION NUMBER: 60/128,898

FILE REPERENCE: 4239-6199

CURRENT APPLICATION NUMBER: 60/128,898

FRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOFTWARE: PALENTH VERSION 3.1

SEQ ID NO 2

LENDRIH: 20 Sequence 42, Application US/10194035

Sequence 42, Application US/10194035

Publication No. US20030144229A1

GENERAL INFORMANTION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE

APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES

APPLICANT: ISHIN Ken

APPLICANT: ISHIN, Ken

APPLICANT: ISHIN, Ken

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

FILE PREPREMENT: 4202-07-12

CURRENT FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: US/10/194,035

CURRENT FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 60/176,115

PRIOR APPLICATION NUMBER: US 60/176,115

PRIOR APPLICATION NUMBER: US 60/176,115

NUMBER: OF SEQ ID NOS: 119

SEQ ID NO 42 0 ö Gaps Gaps FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-540 ö Query Match 100.0%; Score 18; DB 15; Length 20; Best Local Similarity 100.0%; Pred. No. 42; Matches 18; Conservative 0; Mismatches 0; Indels 13; Length 20 Query Match
100.0%; Score 18; DB
Best Local Similarity 100.0%; Pred, No. 42;
Matches 18; Conservative 0; Mismatches ; FEATURE: ; OTHER INFORMATION: Oligonucleotide US-10-068-160-2 1 TGCACCGGTGCAGGGGG 18 3 recaccegracaeeeee 20 TGCACCGGTGCAGGGGGG 20 1 TGCACCGGTGCAGGGGG 18 TYPE: DNA ORGANISM: Artificial Sequence ò d ઠે g

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US-10-666-022-2

j Sequence 2, Application US/10666022

j Sequence 2, Application US/10666022

j Publication No. US20040105872A1

j Publication No. US20040105872A1

j RPDLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services

j APPLICANT: Secretary of the Department of Health and Human Services

j APPLICANT: Verthely1, Daniela

j TITE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

j TITE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

j FILE REFERENCE: 4239-66899

j CURRENT APPLICATION NUMBER: US/10/666,022

j PRIOR FILING DATE: 2002-09-17

j PRIOR FILING DATE: 2002-09-18

j SOFTWARE: Patentin Version 3.1

j SEQ ID NO 2

j LENGTH: 20

mann: 1.
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Sequence 178, Application US/10666022
Publication No. US20040105872A1
GENERAL INPORMATION:
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: APPLICANT: Marrhon of TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISI
TITLE OF INVENTION: WETHOO OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISI
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMELATORY CPG
FILE REPERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR APPLICATION NUMBER: OS 2003-09-18
NUMBER OF SEQ ID NOS: 181
NUMBER OF SEQ ID NOS: 181
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                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42
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Pred. No. 42;
                                                                                                                                                                                     15; Length 20;
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NAME/KEY: misc feature
LOCATION: (1)...(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-2
                                                                                                                                                                               Query Match 100.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 42; Matches 18; Conservative 0; Mismatches
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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US-10-666-022-178
LENGTH: 20
                                                                                                                                                                                  Query Match
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Query Match
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels
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... OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-517
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 517, Application US/09974991C
| Publication No. US20040052763A1
| GENREAL INFORMATION:
| APPLICANT: MOD, JAMES J.
| APPLICANT: MICHAEL
| APPLICANT: FLORA, MICHAEL
| APPLICANT: KLINMAN, DENNIS M.
| TILLE OF INVENTION: IMMUNOSTINULATORY RNA/DNA HYBRID MOLECULES
| FILE REPRENCE: O7787.0042-0
| FILE REPRENCE: 2001-06-07
| FRICH APPLICATION NUMBER: US/09/874,991C
| CURRENT FILING DATE: 2001-06-07
| PRIOR FILING DATE: 2001-06-07
| WUMBER OF SEQ ID NOS: 620
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 517
| LENGTH: 28
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Sequence 525, Application US/09874991C

Publication No. UB20040052763A1

GENERAL INFORMATION:

APPLICANT: MOND, JAMES J.

APPLICANT: MOND, JAMES J.

APPLICANT: KLINMAN, DENNIS M.

TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES

FILE REFRENCE: 07787 .0042-0

CURRENT APPLICATION NUMBER: US/09/874,991C

CURRENT TILING DATE: 2001-06-07

PRIOR PILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 620

SOFTWARE: Patentin Ver. 2.1

SEQ 1D NO 525

LENGTH: 28
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Pred. No. 42;
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100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels
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Matches 18; Conservative 0;
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                     LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                           ; OTHER INFORMATION: synthetic US-10-666-022-178
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US-09-874-991C-517
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SEQ ID NO 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-537
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; Publication No. US20040052763A1
; General information:
    APPLICANT: NOND, James J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: FLORA, MICHAEL
; APPLICANT: FLORA, MICHAEL
; APPLICANT: FLORA, MICHAEL
; TILE OF INVENTION: INMUNOSTIMILATORY RNA/DNA HYBRID MOLECULES
; TILE REPERENCE: 07787.0042-0
; CURRENT FILING DATE: 2001-06-07
; FRIOR PELING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PATENTIN VOY: 2.1
; SEQ ID NO 537
                                        Sequence 529, Application US/09874991C

PUBLIcation No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: MOND, JAMES J.
APPLICANT: KILINMAN, DEBNIS M.
TITLE OF INVERTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: O7787, 0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT PILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 529
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
RESULT 13
US-09-874-991C-529
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Gaps

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3 TGCACCGGTGCAGGGGG 20

1 TGCACCGGTGCAGGGGG 18

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11 TGCACCGGTGCAGGGGGG 28
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RESULT is
US-09-874-991C-548
; Sequence 548, Application US/09874991C
; Publication No. US2004062263A1
; Genence 1. INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: MOND, JAMES J.
; APPLICANT: KLINMAN, DENNIS M.
; TILLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; PILE REFERENCE: 07787-0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; PRIOR FILING DATE: 2000-06-07
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 548
; LINGTH: 40
; TYPE: DNA
; OCHHER INPORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-548
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Search completed: July 2, 2004, 13:58:24 Job time : 139.732 secs

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels

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July 2, 2004, 07:38:45; Search time 1348.02 Seconds (without alignments) 398.746 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-068-160-13 18 1 tgcaccggtgcagggggg 18 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

1: em estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
5: em\_esthum:\*
6: em\_estpl:\*
7: em\_estpl:\*
7: em\_estpl:\*
10: gb\_estp:\*
11: gb\_htc:\*
13: gb\_estp:\*
14: gb\_estp:\*
15: em\_estpl:\*
17: em\_gss\_lnv:\*
18: em\_gss\_lnv:\*
19: e

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		ΩI	100001000	CC11122	AW325275	AQ444154	CB076094
		贸	- 0	7	40	58	14
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91 hj98g11.6 14 hj97e04.3 3 qv76e01.x 25 hk03f05.8 80 zmwnBb02 20 17000687		CC244014 CR261-3F1 CD356849 AGENCOURT CB334319 3529_1 24 B1897515 fm62g02.y AL243778 Tetracodon AL271970 Tetracodon BX26076 BX426076 BX25076 BX426076 CB486533 cmyktptl0 CB016628 pgnlc.pk0	8 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	ANGELOGE TO THE STATE OF THE ST	11129333
- T-4	2 BM621890 8 CC109078 8 CC133230 4 CK151795 9 CNS04021		м, м,	8 AQUS/USB 3 BY315784 4 CD598131 9 CB437108 9 CB182406	AI146003 BF38653 AW26433 BG38138 BF41297 AW024189 CA11114
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#### ALIGNMENTS

LSM Zea mays

Zea mays

Zea mays

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

I Gases it os 840;

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Click,R.W., Numberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: CGDDZ26TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF CG271799 840 bp DNA linear GSS 25-AUG-2003 CG0DZ26TV ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBMa0696F04, genomic survey sequence. CG271799 CG271799.1 GI:34183940 GSS. ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CG271799 LOCUS DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS

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Query Match
Best Local Similarity
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TENU4637 T.cruzi epimastigote normalized cDNA Library Trypanosoma
Cruzi cDNA clone 25h9 5', mRNA sequence.
AW325275
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//organism="Trypanosoma cruzi"
//organism="RWA"
//organism="Cl-Brenner"
// bxref="taxon:5693"
//clone="25b9"
//clone="15b9"
//clone="cDNA liberary constructed with oligo dt primed
//note="cDNA library constructed with oligo dt primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (Pharmacia)"
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Urmenyi, T.P., Rondinelli, E., Pettersson, U., Andersson, B. and
                              1. .840

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/db_xref="taxon:4577"

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/clone="lxmBMa069F04"

/note="voctor: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene survey of the pathogenic protozoan Trypanosoma cruzi
Genome Res. 10 (8), 1103-1107 (2000)
20414748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma cruzi
Trypanosoma cruzi
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum
1 (bases 1 to 245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Aslund L
Contact: Aslund L
Department of Medical Genetics
Uppsala University
Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
Tel: 46 18 471 45 85
Fax: 46 18 52 68 49
Email: lena.aslund@medgen.uu.se
Seg. primer: T7 primer
High quality sequence Brop: 245.
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                                                                                                                                                                                                                  94.4%; Score 17; DB 29; Length 840;
larity 100.0%; Pred. No. 6.3e+03;
Conservative 0; Mismatches 0; Indels
              Location/Qualifiers
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tes 17; Conserv
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/cell type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
HinclI site of the vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
                         GSS 09-JAN-2001
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Hedyotis terminalis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Gentianales, Rubiaceae, Rubioideae,
                                                                                                                                                                                                  Trypanosoma cruzi
Trypanosoma cruzi
Trypanosoma cruzi
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
Trypanosoma; Schizotrypanum.
Trypanosoma; Schizotrypanum.
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma oruzi genome: general Btructure, large gene and repetitive DNA families, and gene discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 14, 2000 this sequence version replaced gi:9372108. Contact: Sanchez D.O. Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aires, Argentina, Trel: (54-11) 4980/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@iib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with crossmatch (see http://genome.washington.edu). Sequences were the trimmed from both ends to remove low quality bases and masked
AV444154
GSSTC0207 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G10L7, genomic survey sequence.
AQ444154
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/clone="G10L7"
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Class: shotgun.
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(NYBG)
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CB087214/c
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Hedyotis centranthoides
Bukarus, Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Bukarus, Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Byermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermacoceae; Hedyotis.

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1 (Dasea; Lo 440)

2 (Dasea; Lo 
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/clone lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/note="Grgan: flower, Vector: pBK-CMV; Site_1: Xho1;
Site_2: EC RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enric
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"
                              l (bases 1 to 319)
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N., O'Shaughnessy, R.L., Balija, V., Martienssen, R.A., McComble, R.W., Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis terminalis flower - Stage (NYBG)
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                                                                                                                                                                                                                                     Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
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Tel: 516 367 8834
Fax: 516 367 8874
Email: mccombie@cehl.org
Plate: hf37 row: c column: 06
Seq primer: -21M13UnivRev
High quality sequence stop:
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Contact: W. Richard McCombie
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Lita Annenherg Hazen Genome Sequencing Center
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PO BOX 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombie@cshl.org
Plate: hj98 row: g column: 11
Seq primer: -21Ml3UnivRev
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/clone="hf37c06"
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Spermacoceae, Hedyotis.
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1 (bases 1 to 50)
Levesque, M. P., T9199, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
                                                                                                                                                                                                                                                                                                             /note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI; Site_2: Eco RI; Date: Completed 12/18/01. Submitted to CSHI_12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2563"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Gentianales, Rubiaceae, Rubioideae,
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Contact: W. Richard McCombie
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Fax: 516 367 8884
Email: mccombie@cebl.org
Plate: hj97 row: e column: 04
Seq primer: -21M13Dinker
High quality sequence stop: 509.
High quality sequence stop: 509.
Location/Qualifiers
1. 509
Armanism="Hedyotis centranthoides"
Armanism="Hedyotis centranthoides"
                                                   1. .440 "organism="Hedyotis centranthoides" |
| mol_type="mRNA" |
| db xref="taxon:219666" |
| clone="hj98g11" |
| dev_stage="pre-anthesis; Stage 2" |
| clone lib="Hedyotis centranthoides fl (NYBG)" |
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/db_xref="taxon:219666"
/clone="hj97e04"
High quality sequence stop: 440.
Location/Qualifiers
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Hedyotis centranthoides
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Hedyotis centranthoides
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
Spermacoceae; Hedyotis.
1 (Bases i to 598)
1 (Bases i to 598)
2 (Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
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ZAMBBD0292G11.f ZMMBBD Zea mays subsp. mays genomic clone
ZAMBBD0292G11 5', genomic survey sequence.
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and Wing,R.
and Wing,R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
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Zea mays subsp. mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae; Zea.
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/clone lib="Hedyotis centranthoides flower - Stage
(NYBG)"
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Contact: W. Richard McCombie
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Tel: 516 367 8874
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hk03 row: f column: 05
Seq primer: -21M13UnivRev
High quality sequence stop: 598.
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/organism="Hedyotis centranthoides"
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/clone="hk03f05"
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                                                                                                                                                                                                                                                                            GV76e01.X1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:1987512 3/
Similar to TR:Q13045 Q13045 FLII ;, mRNA sequence.
A1370313 GI:4149066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNI at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Lengh: 2 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
                                                 Length 509;
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                                                 Score 16.4; DB 14;
Pred. No. 1.1e+04;
0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -40UP from Gibco
High quality sequence stop: 394.
Location/Qualifiers
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                                                 Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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Homo sapiens
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CB087525/c
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/db Xxee="19600449632784"
/clone="19600449632784"
/dav stage="Adult"
/lab_host="Dildo"
/lab_host="Dildo"
/clone=lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mcsquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1:
Not 1 site is 3', Clones available through the Malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                     /sub_species="mays"
/sub_species="mays"
/do xref="taxon:4578"
/clone="xembab0292g11"
/clone_lib="zmMBBb"
/clone_lib="zmMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .684
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
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I (bases 1 to 684)
Holt, R.A., Lin, J.-., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Lin, J.-., H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project Unpublished (2002)
Contact: Holt R.A.
Celera Genomics R.A.
Tels v. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684 bp mRNA linear BST 26-
17000687491457 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
18600449632784 5', mRNA sequence.
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                                                                                                                                                                                                   /organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bmail: HoltRA@celera.com
Plate: NU01004ABX Tow: 1 column: 06
Seq primer: M13 Reverse.
Location/Qualifiers
Tel: 520 626 3967
Fax: 520 621 9288
Baall: http://genome.arizona.edu
PCR PRimers
FORWARD: T7
                                                                                      BACKWARD: M13r
Plate: 0292 row: G column: 11
Seg primer: T7
Class: BAC ends.
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Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ö . 0 Query Match
91.1%; Score 16.4; DB 12; Length
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels

MRZ0160 692 bp mRNA linear EST 25-FEB-2002 17000687442189 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone cDNA 5', mRNA sequence. BM620160

BM620160.1 GI:18918578

Anopheles gambiae (African malaria mosquito) Anopheles gambiae Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

E 1 [bases 1 to 692]
S Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charler, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celara Anopheles gambiae EST project
Unpublished (2002)
Conteat Genomics
Conteat Genomics
Tel: 240453151
Fax: 240453480
Email: HoltRA@celara.com
Plate: NU01004ABH row: H column: 12
Seq primer: MIR Reverse
Seq primer: MIR Reverse

Location/Qualifiers

/organism="Anopheles gambiae" /mol\_type="mRNA" /strain="RSP-ST (Reduced susc. to Permethrin - std.

/db xref="teaxon:7165"
/clone="1560044568094"
/clone="1560044568094"
/dev grage="Adult"
/lab host="Dhlu"
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/clone lib="A.Gam.ad.cDNA1"
/clone lib="A.Gam.ad.cDNA1"
/clone lib="A.Gam.ad.cDNA1"
/clone lip="A.Gam.ad.cDNA1"
/clone li

•• • ch 91.1%; Score 16.4; DB 12; Length 692; 1 Similarity 94.4%; Pred. No. 1.1e+04; 17; Conservative 0; Mismatches 1; Indels 0; Query Match Best Local Similarity

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BM621890 708 bp mRNA linear EST 25-FBB-2002 17000687447901 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449620865 5', mRNA sequence.

BM621890 ACCESSION

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Library was provided by David Severson
Seg primer: T7
Class: BAC ends.
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CC109078
GC109078.1 GI:29978133
GSS.
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
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                                                             Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles
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/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
                                                                                                                                                                                                                       1 (bases 1 to 708)

10 (bases 1 to 708)

Charlab,R., Lin,J.-d., Murphy,S.D., Evans,C.A., Kraft,C.L.,

Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.

Celera Anopheles gambiae EST project

Contact: Holt R.A.

Celera Genomics
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1981: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
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1 (bases 1 to 779)
Loftus, B., Shetty, J., Kmudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other 26Ses NDL.50B23.SP6
Contact: Brandan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 w. Gude Dr., Rockville, MD 20850, USA
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU10404MBU row: H column: 15
Seq primer: M13 Reverse.
Location/Qualifiers
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Aedes aegypti
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      GI:18920308
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/clone="Volute Dame Liverpool"
/note="vector: pECBAC1; Site_1: Hind III; The library was
/repared from whole body tissue of newly hatched Lil larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
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Neoptera; Endopterygota; Diptera, Nematocera; Culicoidea; Aedes;
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91.1%; Score 16.4; DB 28; Length 799;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0
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Fax: 301-838-0208
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1 (bases 1 to 799)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypt;
Unpublished (2003)
Other GSSs: NDL.50B22.SP6
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Library was provided by David Severson
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Class: BAC ends.
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/organism="Aedes aegypti"
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RESULT 15 CK151795/c

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Query Match Best Local Similarity 94.4%; Pred. No. 1.18+04; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps

ORIGIN

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Search completed: July 2, 2004, 13:32:56 Job time : 1351.14 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Kun on:	July 2, 2004, 07:36:05 ; Search time 563.317 Seconds (Without alignments) 1231.080 Million cell updates/sec	
Title: Perfect score: Sequence:	US-10-068-160-15 16 1 999catgcatggggg 16	
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched:	3470272 segs, 21671516995 residues	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	i	90	Si	ne un	anı	anie	Z .	AC139423 CANIS LAM	2 1	18 L	AC147160 Mus muscu	attus n	ACI31337 Mus muscu	AXZSI652 Sequence	SELEFOIS	U51741 IDOGOGA tri	AF032369 Cochliobo	AF032368 Cochliobo	X76056 N. sylvestr	ASSEL4 B.Bacchari	AC079003 Homo sapi	AC073133 Homo sapi	AL669986 Neurospor	AL359538 Human UNA	AC145324 Orvza sat	AP001068 Homo sapi	AL773602 Homo sapi	AC112907 Homo sapi	ALBUBOSH OLYZA SAC	AP001067 Homo sapi	AC106881 Homo sapi	AL136160 Human DNA	AY178791 Canis fam	OHO	0 0			.49 Homo	AC133160 Mus muscu AC023222 Homo sapi				linear	S SEQUENCE SAMPLING.				ebrata, Buteleos	Muridae; Murinae;	Lander, E.		
SUMMARIES	B 1D																																							2 AC133160 2 AC023222		ALIGNMENTS		10	116K23, LOW	29532	•	mouse}	Chordata	kodencia; )	, Nusbaum, C. and	745-110W	
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TITLE

COMMENT

E Libraes I to 65655 And Alber, B. Ali, A. Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAtellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Govette, M., Graham, L., Grand-Pierre, N., Edock, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, R., Johnson, R., Landers, E., Kanata, A., Kalis, G., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, R., Macdonald, P., Major, J., Marquis, M., Matthews, C., Macdonald, P., Major, J., Marquis, J., Matthews, C., Macdonald, P., Major, J., Maldrim, J., Matthews, C., Macdonald, P., Major, J., Mardonall, P., Mickernan, R., Maldrim, J., Matthews, C., Morbu, C., Norman, C.H., O'Connor, T., Maldrim, J., Matthews, C., Morbu, C., Norman, C.H., O'Connor, T., O'Domell, P., Petre, S., Schupback, R., Saymond, C., Retta, R., Petra, R., Spencer, B., Satros, T., Schupback, R., Stander, S., Schubback, S., Schupback, S., Stander, S., Schupback, R., Stander, S., Schuback, S., Schubback, S., Stander, S., Schuback, S., Stander, S., Schuback, S., Stander, S., Schuback, S., Stander, S., Schuback, S., Schuback, S., Stander, S

\* sequencing reads that have not been assembled into \* contigs. Runs of N are used to separate the reads \* and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for \* identifying clones that may be gene-rich and allows \* overlap relationships among clones to be deduced. \* However, it should not be assumed that this clone \* will be sequenced to completion. In the event that the record is updated, the accession number will \* be preserved. NOTE: This record contains 81 individual

contig of 710 bp in length gap of 100 bp contig of 715 bp in length contig of 722 bp in length gap of 100 bp contig of 707 bp in length gap of 100 bp contig of 707 bp in length gap of 100 bp contig of 719 bp in length contig of 719 bp in length contig of 719 bp in length 100 bp of 726 bp in length 100 bp of 710 bp in length in length 100 bp of 715 bp in length 100 bp of 702 bp : 100 bp of 684 bp 100 bp of 709 100 bp contig of 0 gap of 100 contig gap of 710: 810: 1525: 1625: 2347: 22447: 32554: 39499: 40699: 40689: 5594: 5694: 6378: 6478: 7188: 8003: 8103: 8805: 7288: 111 16266 23448 332155 24448 332155 24448 25595 25695 25795

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Mus musculus clone RP24-566122, WORKING DRAFT SEQUENCE, 6 unordered
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Birren, B., Nusbaum, C. and Lander, E.

Mus musculus, clone RP24-566J22

Unpublished
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39704: gap of 100 bp 40523: contig of 719 bp in length 41522: contig of 719 bp in length 41522: contig of 729 bp in length 42168: gap of 100 bp 42268: contig of 716 bp in length 42588: contig of 716 bp in length 43702: contig of 717 bp in length 44539: contig of 717 bp in length 44539: contig of 717 bp in length 44539: contig of 717 bp in length 4559: gap of 100 bp 454539: contig of 726 bp in length 45639: gap of 100 bp 454539: contig of 726 bp in length 45639: gap of 100 bp 454539: contig of 716 bp in length 47800: contig of 716 bp in length 48415: gap of 100 bp 48405: gap of 100 bp 50139: contig of 718 bp in length 48415: gap of 100 bp 50139: contig of 718 bp in length 50139: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 718 bp in length 5186: gap of 100 bp 50139: contig of 708 bp in length 5184: contig of 708 bp in length 5184: contig of 708 bp in length 55534: contig of 708 bp in 
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HTG; HTGS PHASB1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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                                                         pieces.
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AC118209/c
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SOURCE
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TITLE
JOURNAL
REFERENCE
AUTHORS
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Direct Submission

Submitted (14.*AP-2002) Whitehead Institute/MIT Center for Genome States 23 (Dases 1 to 14973)

Research, 320 Charles Street, Cambridge MA 02141, USA

(Dases 1 to 14973)

Research, 320 Charles Street, Cambridge MA 02141, USA

(Dases 1 to 14973)

Research, 1 Charles Street, Cambridge MA 02141, USA

Research, 2 Charles Street, Cambridge MA 02141, USA

Collymore, M. Wubbaum, C. Lander, E. & Abouellaid, A. & Bloom, T. & Anderson, S. Arzedhchif H. M. Barna, N. Bastien, V. Bloom, T. & Collymore, M. Dodge, S. M. Docke, K. Dorris, D. Charles Jan. Charg, J. Charg, J. Charles, D. Diaz, J.S. & Collymore, M. Card, Parc, S. & Gahan, J. & Rad, M. & Parc, S. & Gahan, J. & Rad, M. & Relis, C. & Lander, R. Machen, R. & Machen, C. & Macdonal, P. & Machen, M. & Machen, R. & 
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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JOURNAL
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FEATURES

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Direct Submission

Submitted (27-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Selvania, Sanchelli, M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Canarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Daztellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Farzeras, P., FitzGerald, M., Gage, D., Galdagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landerst, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maciean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nouly, M., Najor, J., Schauer, S., Schauer, 
                                      McCarthy, M. Meldrim, J. Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., Morcon, T., O'Vonnell, P., O'Nell, D., O'Iver, J., Reterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P., Senti, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vas. Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: NIBR
Web site: http://www-seq.wi.mit.edu
Conteart: sequence submissionsogenome.wi.mit.edu
Conteart: sequence submissionsogenome.wi.mit.edu
Conteart: sequence submissionsogenome.wi.mit.edu
Center project name: L27131
Center clone name: 27 A L1
Consensus vector: plasmid; n/a; 100% of reads
Assembly program: plasmid; n/a; 100% of reads
Assembly program: plasmid; n/a; 100% of reads
Consensus quality: 151397 bases at least Q40
Consensus quality: 152629 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 155000; agarose-fp
Quality coverage: 10.5 in Q20 bases; sum-of-contigs
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           Macdonald, P., Major, J., Matthews, C.,
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660: gap of 100 bp
2921: contig of 2261 bp in length
3021: gap of 100 bp
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Mus musculus clone RP24-227A11, WORKING DRAFT SEQUENCE, 9 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 154143)
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Birren, B., Nusbaum, C., Lander, E., Bouslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P. FitzGerald, M., Gage, D., Galagan, J., Gard, S., Grands, S., Gord, S., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                  1 27796: contig of 27796 bp in length 797 27886: gap of 100 bp 897 33321: contig of 5428 bp in length 322 33421: gap of 100 bp 422 45008: contig of 12487 bp in length 909 46008: gap of 100 bp 64008: gap of 100 bp 64008: gap of 100 bp 746008: gap of 100 bp 746009: gap of 100 bp 749773: contig of 45164 bp in length 190009: location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="Lexon:10090"
/clone="RP24-566222"
/clone lib="RPCI-24 Male Mouse BAC"
1. 27796
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/note="assembly_fragment"
85346. .130509
/note="assembly_fragment"
130610. .14973
/note="assembly_fragment"
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34422. .45908
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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Les 16; Conservative
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46509
85246
85346
130510
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Query Match

ORIGIN

Matches

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS

DEFINITION

RESULT 3 AC131924

g

ACCESSION

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Sidjanin, D.J., Miller, B., Kijas, J., McElwee, J., Pillardy, J., Malek, J., Pai, G., Feldblyum, T., Fraser, C., Acland, G. and Aguirre, G. Malek, J., Pai, G., Feldblyum, T., Fraser, C., Acland, G. and Aguirre, G. Direct Submission

Submitted (14-NOV-2002) James A. Baker Institute for Animal Health, Cornell University, Mungerford Hill Rd., Ithaca, NY 14853, USA * NOTE: This is a 'working draft' sequence. It currently * consists of 55 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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g of 1209 bp in length
if unknown length
of 814 bp in length
of unknown length
ig of 948 bp in length
of unknown length
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g of 851 bp in length
unknown length
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of 1909 bp in length
unknown length
of 1682 bp in length
unknown length
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f unknown length
g of 966 bp in length
f unknown length
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of 1809 bp in length
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2019 bp in length
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HTG; HTGS PHASE1.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
Hammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
Sidjanin, D.J., Miller, B., Kijas, J., McElwee, J., Pillardy, J., Malek, J., Pai, G., Feldelyum, T., Fraser, C., Acland, G. and Aguirre, G. Radiation hybrid map, physical map, and low-pass genomic sequence of the canine prod region on CFA9 and comparative mapping with the Syntemic region on human chromosome 17
E 22508185
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/note="assembly_fragment
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0;
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70465. .100316
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-227A11"

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
I (bases 1 to 158920)

A khter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Hadhighi, P., Han, J., Hangen, N., Ho, S.-L., Idol, J.R., Karlins, E., Harting, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Masteri, B., McDowell, J., Paguirigan, C., Pearson, R., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P. J., Touchman, J.W., Vogt, J.L., Netherby, K.D., Higglis, L., Young, A. and Green, E.D.
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Submitted (25-OCT-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 158920)
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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HTG; WINGS PHASE2; HTGS_DRAFT.
Canis familiaris (dog)
Canis familiaris
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42358: contig of 2189 bp in length 44295: gap of unknown length 44295: gap of unknown length 44295: gap of unknown length 45295: gap of unknown length 45295: gap of unknown length 49310: contig of 3182 bp in length 49530: gap of unknown length length 52462: gap of unknown length length 52362: contig of 2832 bp in length 52362: contig of 2832 bp in length 52362: contig of 2832 bp in length 59167: gap of unknown length 1978: contig of 292 bp in length 59167: gap of unknown length 65069: gap of unknown length 65169: gap of unknown length 77011: gap of unknown length 77334: gap of unknown length 77334: gap of unknown length 87511: gap of unknown length 87511: gap of unknown length 87511: gap of unknown length 92611: contig of 3812 bp in length 92611: contig of 3829 bp in length 92611: contig of 4386 bp in length 92611: contig of 3829 bp in length 92611: gap of unknown length 97597: gap of unknown length 114333: gap of unknown length 114339: gap of unknown length 114399: gap of unknown length 114990: gap of unknown length 114990: gap of un
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tive 0; Mismatches 0; Indels
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    157263
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/db_xref="taxon:9615"
/chromosome="CFA9"

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136826
136926
145361
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AC135955 158920 bp DNA linear HTG 14-NOV-2002 Canis familiaris clone RP81-65H2, WORKING DRAFT SEQUENCE, 3 ordered pieces.

DEFINITION RESULT 5 AC135955

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source

ORIGIN

FEATURES

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

1 (bases I to 18340)

1 (bases I to 183540)

2 Akhter,N., Antonellia,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J., Haphighi,P., Han,J., Hangen,N., Ho,S.-L., Idol,J.R., Karlins,B., Laric,P., Le-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Magnirigan,C., Pearson,N., Portnoy,M.B., Nacowell,J., Pagnirigan,C., Pearson,R., Portnoy,M.B., Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C., Stantrapop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vongt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,B.D.
                                                                                                                                                                                                                                                                                    AC139123 183540 bp DNA linear HTG 05-FEB-2003
Canis familiaris clone RP81-340C22, WORKING DRAFT SEQUENCE, 10
ordered pleces.
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Sequencing vector: plasmid; n/a; 100% of reads (Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap, version 0.990319 Consensus quality: 181869 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-FBB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Feb 5, 2003 this sequence version replaced gi:27884878.

Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (24-JNA-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 183540)
                                                                                                Gaps
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                                                Length 165077;
                                                                                                0; Indels
                                                Query Match
100.0%; Score 16; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc zco@nhgri.nih.gov
Center project Information
Center project name: eav
Center clone name: 340022
                                                                                                                                                                                                                                                                                                                                                                                                         AC139123.2 GI:28209437
HTG; HTGS PHASE2; HTGS_DRAFT.
Canis familiaris (dog)
Canis familiaris
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2 (bases 1 to 183540)
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                                                                                                                                                                                                                                                                RESULT 7
AC139123
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MCPherson, J. D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
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Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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McPherson.J.D.
Direct Submission
Submitted (26-SEP-2001) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, Missouri 63108, USA
J (bases 1 to 165077)
McPherson,J.D. and Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC084382 165077 bp DNA linear Mus musculus clone RP23-5K17, complete sequence. AC084382 GI:15778814 HTG.
1 37538: contig of 37538 bp in length 37539 37638: gap of unknown length 37639 136759: contig of 99121 bp in length 136760 136869; gap of unknown length Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                    1. 158920
| organism="Canis familiaris"
| /mol_type="genomic DNA"
| /db_xref="taxon:9615"
| /clone="RP81-65H2"
| /clone=lib="RP81"
| 1. 37538
| /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                      vector side:left"
37639. 136759
/note=massembly_fragment"
136860. 158920
/note=massembly_fragment
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us-10-068-160-15.rge
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* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1319: contig of 1319 bp in length 1310 1419: gap of unknown length 6512 6611: contig of 1309 bp in length 6512 6611: gap of unknown length 1300 1409: contig of 13139 bp in length 6612 17980: contig of 43459 bp in length 61639: gap of unknown length 116779 116779: contig of 15127 bp in length 116779 116779: contig of 15137 bp in length 116779 116779: contig of 15137 bp in length 116779 116779: contig of 2513 bp in length 116879 116779: contig of 2513 bp in length 1168907 1183540: contig of 2513 bp in length 1168907 1183540: contig of 2513 bp in length 1168907 1183540: contig of 14534 bp in length 1168907 1183540: contig of 2513 bp in length 1168907 1183
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1.138606
1note="clone overlaps with GenBank Accession Number AC135955 clone RP81-65H2 (center project name cw1)"
Consensus quality: 182282 bases at least Q30
Consensus quality: 182531 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 182640; sum-of-contigs
Quality coverage: 11.73x in Q20 bases; sum-of-contigs
Quality coverage: 11.77x in Q20 bases; sum-of-contigs

    183540
    organism="Canis familiaris"

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18081. .61539

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61640. .101551

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116872. .115772

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116873. .115772

/note="assembly_fragment"

116873. .115772
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note="assembly_fragment"
[69007, 183540
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Length 183540;

100.0%; Score 16; DB 2; I 100.0%; Pred. No. 1.1e+02;

Query Match Best Local Similarity

ORIGIN

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Submitted (28-40G-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
CB 3 (bases 1 to 186129)
Sirent, M. Wisbaum, C. Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Cock, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Paro, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Ganath, J., Hulme, W., Higez, N., Hagopian, D., Hagos, B., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacCarthy, M., Maddnald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Nguyen, C., Nicol, R., Mihova, T., Manning, V., Murphy, T., Naylor, J., Peterson, R., Phunkhang, P., Pierre, N., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Reymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataman, V., Wiell, R., Volan, A. and Zody, M. Direct, Submission, M., Mann, D., Young, G., Zainmen, J., Zainmer, A., and Zody, M. Direct, Submission, M., Mann, D., Young, G., Mann, D., Young, G., Lander, J., Sambek, L., Zainmer, A., and Zody, M., Direct, Submission, M., Mann, D., Young, M., Mann, M., Mann, D., Young, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M.,
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1. (Dases I to 186129)

2. (Dases I to 186129)

Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Boguslavkiy, L., Boukhgalter, B., Camarata, O., Chang, J., Dokrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gerdam, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartes, A., Kalls, C., Landers, T., Levine, R., Jones, C., Kamat, A., Kartes, A., MacLean, C., Macdonald, P., Major, J., Mathews, C., McChan, C., Macdonald, P., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicoll, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zammer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                   AC131987 196129 bp DNA linear HTG 27-MAR-2003 Mus musculus clone RP24-184L10, WORKING DRAFT SEQUENCE, 8 unordered
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 186129)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Gaps
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    Indels
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HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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    Mismatches
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Gaps

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CNSO1RHC
Human chromosome 14 DNA sequence BAC R-736N17 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryosational Eukarota, Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryosa; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 19462) Brimates; Catarrhini; Hominidae; Homo. Heliig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : R-45P15 (AC-AL138976) Ownstream BAC (overlapping the SP6 end) : C-2538G10
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap, version 2.0
Quality coverage: 10.43x in Q20 bases; sum-of-contigs
                     Indels
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
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/note="watching EMBL:G04572
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/clone_lib="RPCI-11"
                                                                                                                173050 descarecarececes 173035
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Range : bases
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AL161669.5 GI:13990665
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2 (bases 1 to 192462)
                                                                    1 GGGCATGCATGGGGGG 16
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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                        16; Conservative
  Best Local Similarity
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TITLE
JOURNAL
                          Matches
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AUTHORS
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CNS01RHC
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                                                                                                             셤
  ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project name: L27107
Center clone name: StaTistics
Sequencing vector: Plasmid; n/s: 100% of reads
Cenmistry: Dyo-terminator Big Dyo; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 184631 bases at least Q30
Consensus quality: 185040 bases at least Q20
Innert size: 168000; agarose-fp
Innert size: 188429; sum-of-contigs
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                 work: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1963: contig of 1963 bp in length
1964 2063: gap of 100 bp
2064 7095: contig of 5032 bp in length
7195: gap of 100 bp
7196: 20081: contig of 5032 bp in length
7196: 20081: contig of 12886 bp in length
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2510: 32609: gap of 100 bp
2510: 45123: contig of 12514 bp in length
7514 45223: gap of 100 bp
73181: contig of 27958 bp in length
73181: contig of 93754 bp in length
73281: gap of 100 bp
73281: gap of 100 bp
73281: gap of 100 bp
73282: 167035: contig of 93754 bp in length
73381: gap of 100 bp
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1. 1963
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15224. .73181
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100.0%; Score 16; DB 2; Length 186129;

Query Match

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RHdb:RH53929
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Identified using the e-PCR software (G. Schuler) "
103114. . 103373
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ö Gaps ö Length 192462; Query Match
100.0%; Score 16; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels

ORIGIN

COMMENT

99243 GGCCATGCATGGGGGG 99258 16 1 GGCCATGCATGGGGGG જ

DEFINITION AC123656 LOCUS

AC123656 222510 bp DNA linear HTG 27-MAR-2003 Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered AC123656.6 GI:29294284 HTG; HTGS\_PHASE1; HTGS\_DRAFT. Mus musculus (house mouse) Mus musculus VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Bases I to 222510)
Birren, B., Nusbaum, C. and Lander, E.
Harm, B., Clone RP23-198M21 Unpublished REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

unquantibles

Chases I to 222510)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,M., astien,V., Bloom,T., Boguslawiy,L., Changelo,M., Campopiano,A., Chang,J., Chagaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Devarlano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Erreira,P., FitzGerald,M., FitzHup,M., Gage,D., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Grahan,L., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Grahan,L., Gardyna,S., Hotton,L., Hulme,W., Iliev,T., Usonson,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,M., Matchews,C., McCarthy,M., McCapan,P., McCernan,R., Meldrim,J., Norbu,C., Norman,C.H., O'Connoll,P., O'Donnell,P., Norbu,C., Norman,C.H., O'Connoll,P., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Ray,A., Santos,R., Schauer,S., Schubback,R., Schauer,S., Schubback,R., Seaman,S., Sovery,P., Spencer,B., Stange-Thomann,N., Schubback,R., Stange-Thomann,N., Stojanovic,N., Strawers,M., Travis,N., Trigillio,J., Vassillev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

Direct Submission Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 222510) TITLE JOURNAL

REFERENCE

ks birren, B. Nuesamm,C., Lander, E., Aboustlell, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastisn, V., Bloom, T., Boukhgalter, B., Gamarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, M., Cooke, P., Cortum, B., DeArellano, K., Dolaz, J.S., Dooley, K., Dorris, L., Brickson, J., Faro, S., Ferreira, P., PitzGerald, W., Gage, D., Gajagan, D., Hagopian, D., Hagopian, D., Hagopian, D., Hagopian, D., Hagopian, J., Cardyna, S., Indefers, L., Laule, R., Marler, M., Marler, M., Marchie, R., Marcher, J., Monnson, R., Jones, C., Macdonald, P., Majori, M., Manbitt, R., Maccarth, M., Marchews, C., McCarth, M., Mayora, T., Morbu, C., O'Comnor, T., O'Comnell, P., Major, J., Schupback, R., Saman, S., Severy, P., Smith, C., Stange-Thomann, M., Schupback, R., Saman, S., Severy, P., Smith, C., Marchews, M., Marchews, M., Mayora, T., Woung, G., Zamoun, J., Zembek, L., Zimmer, A. and Zody, M., Myman, D., Young, G., Zamoun, J., Zembek, L., Zimmer, A. and Zody, M., Wassillack, H., Wassagar, M., Takers, M., Takers, M., Takers, M., Takers, M., Marchews, M., M TITEE JOURNAL AUTHORS

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

2031: contig of 2031 bp in length 2131: gap of 100 bp 15244: contig of 13113 bp in length 15344: gap of 100 bp 3749: contig of 22305 bp in length 37749: gap of 100 bp 148102: contig of 110353 bp in length 148202: gap of 100 bp 190361: contig of 42159 bp in length 190461: gap of 100 bp 222510: contig of 32049 bp in length Location/Qualifiers 2032 2132 15245 15345 37650 37750 148103 190362 FEATURES

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Best Local Similarity 100.0
Matches 16; Conservative
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111449
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20355
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Wilson,R.X.
Wilson,R.X.
Submission (04-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 227805)
Wilson,R.K.
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                                                                                                                                                                                                                          Query Match 100.0%; Score 16; DB 2; Length 222510; Best Local Similarity 100.0%; Pred. No. 1.18+02; Matches 16; Conservative 0; Mismatches 0; Indels 0;
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
                                          /note="assembly_fragment"
2132. .15244
/note="assembly_fragment"
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                                                                                                                                                         234548 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-8K1, WORKING DRAFT SEQUENCE, 2
unocédered pieces.
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                        AC095635.6 GI:30467118
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus noivegicus (Norway rat)
50847 GGCATGCATGGGGGG 50832
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Eouston, TX 77030, USA

CES 3 (bases 1 to 214548)

Rat Genome Sequencing Consortium.

Direct Submission

AL Submission

AL Submitted (19-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24817791.

The sequence in this assembly is a combination of BAC based reads and whole genome shortun sequencing reads assembled using Atlas (Ihttp://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence.
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered
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Consensus quality: 224642 bases at least Q30
Consensus quality: 225972 bases at least Q30
Estimated insert size: 2222080; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Query Match

Best Local Similarity 100.0%; Pred. No. 1.16+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0;
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/organism="Rattus norvegicus"
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/db xref="taxon:10116"
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AC131337
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
not known and their order in this sequence record is
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282339: contig of 46274 bp in length
282339: gap of 100 bp
325240: contig of 42901 bp in length
355340: gap of 100 bp
345420: contig of 20080 bp in length.
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gap of 100 bp
contig of 10555 bp in length
gap of 100 bp
contig of 20133 bp in length
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contig of 75941 bp in length
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gap of 100 bp
contig of 35527 bp in length
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contig of 33201 bp in length
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/note="assembly_fragment"
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/note="assembly_fragment'
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|note="assembly_fragment"
|40334. .166937
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/db_xref="taxon:10090"
/clone="RP23-480E1"
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235865: 9
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Direct Submission
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 345420)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-480E1
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 345420)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L26504
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                   AC131337
AC131337,4 GI:30017797
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
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COMMENT

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The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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S21226739FB10.T0 CZECHII/Ei Mus musculus STS genomic, sequence
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tive 0; Mismatches 0
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Wood, L.S., Voge...
Wang, J. and Liu, D.
Human ion channels
Lostent: WO 0.16849-A 47 20-SEP-2001;
Pharmacia & Upjohn Company (US)
Location/Qualifiers
657
""Jomo sapiens"
           235966. .282239 / note="assembly_fragment" 282340 .325240 / note="assembly_fragment" 325341 .345420 / note="assembly_fragment" clone end:T7 vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 47 from Patent WO0168849.
AX251652
'note="assembly_fragment"
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Whitehead Institute for Biomedical Research, Center for Genome Research and Charles Street, Cambridge, MA 02141, USA Tel: 6172821477

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Pars (17282147)

Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 867

Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 12921/5vium, C3H/Hebr, and BAIRG-CBW. The WGS
were generated from 12921/5vium, C3H/Hebr, and BAIRG-CBW. The WGS
were generated from 12921/5vium, C3H/Hebr, and BAIRG-CBW. The WGS
were generated from the SSSI/Svium, C3HL/GJ assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
anotated an STSS and 81,000 SNPs were annotated with alleles from C57BL/GJ
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.

| Insert Cort these SNPs was estimated at approximately 98%.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	TOTOTE	Aad17168 Human ion	Acd01553 cDNA clon		Ada72822 Rice gene	Aal31444 Human SNP	Abl78599 Human ova	Aag22507 Lys64, Pr		Aag22510 Insert fr	Aag22506 Lys64, Pr		Ach33855 Human end	Aav33946 Gibbon in		Aan92339 Single st	Abq54810 Human ova	Aat84711 Human Shc	Aas94988 Human DNA	Acd19383 cDNA enco	Abl69709 Prostate	Abt10905 Human bre	Adb70327 Keratin 5	Adb75393 Prostate
SUMMARIES		AAD17168	ACD01553	ADE29244	ADA72822	AAL31444	ABL78599	AAQ22507	AAQ22508	AAQ22510	AAQ22506	ACH19351	ACH33855	AAV33946	AAN80502	AAN92339	ABQ54810	AAT84711	AAS94988	ACD19383	ABL69709	ABT10905	ADB70327	ADB75393
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Aaz24613 Human lun	Aac65852 Human lun	Abl49071 Human lun	Abg92257 Human lun	Ada28206 Human lun	Ade53411 Human lun	Ade56166 Human gen		Acd19382 cDNA enco	Abk94721 Neurodege	Add14725 Human src	Human	Aas30132 Human lun	Adb33469 Human nov	Aas30131 Human lun	Adb33468 Human nov	Aag82848 P-selecti	Aaa34926 Human ade	Aaf21048 Human low	Abz96742 Human nuc	Aas30133 Human lun	Adb33470 Human nov
AA224613	AAC65852	ABL49071	ABQ92257	ADA28206	ADE53411	ADE56166	ADD45277	ACD19382	ABK94721	ADD14725	ABA20059	AAS30132	ADB33469	AAS30131	ADB33468	AAQ82848	AAA34926	AAF21048	ABZ96742	AAS30133	ADB33470
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#### **ALIGNMENTS**

RESULT 1

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Human, ion channel-91, ion91; antiinflammatory; immunosuppressive; analgesic; nootropic, neuroprotective; antidepressant; cardiant; cytostatic, antiviral; human immunodeficiency virus; HIV; anorectic; antiviral; thyroid disorder; thyrotoxicosis; myxoedema; renal failure; Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke; psychotic disorder; neurological disorder; anxiety; dyskinesia; Huntington's disease; degenerative disorder; Parkinson's disease; schizophrenia; Alzheimer's disease; cardiovascular disease; cancer; metabolic disorder; anorexia; obesity; mental disorder; ss.
                                                                                                                                                                                                                                                                                                                                        /*tag= a /product= nfuman ion91 protein" /product= "fuman except= (pos:333. .341, aa:Ser-Pro) /rans1 except= (pos:334 in-frame stop codon insertion; CDS does not include start /partial
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                    Human ion channel-91 (ion91) cDNA.
               В.
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10-MAR-2000; 2000US-0188518P.
10-MAR-2000; 2000US-0188519P.
06-JUL-2000; 2000US-0218815P.
06-JUL-2000; 2000US-0216481P.
AAD17168/c
ID AAD17168 standard; cDNA; 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001; 2001WO-US007503.
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                        29-NOV-2001
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                                            AAD17168;
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WPI; 2003-313250/30.

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The patent discloses novel human ion channel polypeptides and their corresponding polymucleotides. The ion channel sequences and their modulators are used for the treatment of viral infections (e.g. human immunodeficiency virus (HVV), thyroid disorders (e.g., thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g., thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g., thyrotoxicosis, psychotic and neurological disorders (e.g. auxiety, depression and schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative disorders (e.g., Parkinson's disease, Alzheimer's disease), cardiovascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity) and mental disorders. The present sequence is a cDNA encoding human ion channel-91 (ion91) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ion channel; immune response; RFLP; genetic mapping; restriction fragment length polymorphism; viral infection; inflammatory condition; Crohn's disease; homestaals; cancer; rheumatoid archritis; autoimmune disorder; CMS disorder; decential nervous system disorder; Huntington's disease; virucide; degenerative disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disease; myocardial infarction; hormonal disorder; irranscription factor; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; nootropic; anticonvulsant; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                Vogeli G, Karnovsky AM, Ruble CL, Linske-O'connell LI,
                                                                                                                            New ion channel polynucleotides and polypeptides, useful for identification of ion channel modulators and treatment of mental disorders, infections, cancer and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.8%; Score 15; DB 4; Length 657; Best Local Similarity 100.0%; Pred. No. 4.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; cardiant; gene; ss.
                                                                                                                                                                                                            Claim 3; Page 99; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553/c
ACD01553 standard; cDNA; 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2-SEP-2002; 2002WO-US029087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0318733P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 GGGCATGCATGGGGG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCATGCATGGGGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2003 (first entry)
                                                                         2001-565795/63.
                                                                                             P-PSDB; AAE10116.
                                  Liu D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001;
13-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberds SL,
                  Wood LS,
Wang J, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD01553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACD01553,
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The present invention relates to the isolation of novel human ion channel polypeptides, and the polynucleotide sequences encoding them. The human ion channel polypeptides are useful for inducing an immune response in a mammal, and for identifying a compound which binds to and/or modulates the on channel. The polynucleotide sequences encoding human ion channel polypeptides are useful for screening restriction fragment length polynucleotides are useful in the blanch of diseases or conditions and to genetic mapping. The human ion channel polypeptide and polynucleotide sequences or useful in the treatment of diseases or conditions such as viral infections, inflammatory conditions (e.g. Crohn's disease), diseases central nervous system (NNS) disorders (e.g. dementia, Huntington's disease), degenerative disorders (e.g. mycandial infarction), cancer, and hormonal disorders. The polynucleotide sequences are useful to design novel transcription factors for modulating the expression of human ion them. The present sequence represents a cDNA clone encoding a human ion channel polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neuroprotective; neuroleptic; immunosuppressive; cardiant; antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic; opthalmological; cytostatic; hypertensive; hypotensive; vasotropic; antidiyraine; analgesic; antiparkinsonian; thrombolytic; antithyroid; ion channel; ion-x; brain disorder; mental disorder; schizophrenia; depression; anxiety; attention deficit hyperactivity disorder; migraine; stroke; neurodegenerative disease; Alzheimer's disease; parkinson's disease; glaucoma; macular degeneration; earliorascular disease; ischeemia; cogeneration; high blood pressure; restenosis; thyroid disorder; renal failure; inflammatory condition; autoimmune disorder; rheumatoid arthritis; movement disorder; cardiovascular disorder; thrombosis; athersclerosis; proliferative disorder; cardiovascular disorder; hormonal disorder; sexual dysfunction;
                                                             Novel human ion channel polypeptide, useful for inducing an immune response in a mammal and for treating disease or conditions related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 15; DB 7; Length 657; 100.0%; Pred. No. 4.5e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human ion channel ion-91 cDNA.
                                                                                                                                                     Example 1; Page 103; 146pp; English.
                                                                                                          central nervous system and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
ADE22244/c
ID ADE29244 standard; cDNA; 657 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 eeecarecareeeee 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGCATGCATGGGGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.89
Best Local Similarity 100.3
Matches 15; Conservative
                       P-PSDB; ABU97377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003190714-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE29244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; ss
%XCCCCCCCCCCCCCCX
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The invention describes an isolated nucleic acid comprising a sequence encoding at least a portion of an ion channel (ion-x). The invention is useful to detect and treat diseases and conditions of the brain, particularly mental diseases and conditions of the brain, anxiety, attention deficit hyperactivity disorder, migraine, stroke, and neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease, glaucoma and macular degeneration, cardiovascular diseases such as ischaemia, congestive heart failure, arrythmia, high blood pressure and sectenosis. The invention may also be used to detect or treat thyroid disorders, renal failure, inflammatory conditions, autoimmune disorders including zheumatoid arthritis, movement disorders, central nervous system disorders, infections, eating disorders, cardiovascular disorders including thrombosis and athersclerosis, and proliferative disorders such as cancers, hormonal disorders and sexual dysfunction. This sequence encodes a novel ion channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid sequences encoding ion channels are useful to detect and treat human diseases and conditions, particularly of the brain, especially mental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 9; Length 657;
Pred. No. 4.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    Roberds SL, Benjamin CW, Karnovsky AM, Ruble CL;
Linske-O'connell LI, Wang J, Liu D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 47; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; Poses 15; Conservative 0;
            10-MAR-2000; 2000US-018846PD.
10-MAR-2000; 2000US-018846FP.
10-MAR-2000; 2000US-0188517P.
10-MAR-2000; 2000US-0188518P.
10-MAR-2000; 2000US-0188518P.
05-UJL-2000; 2000US-02154515P.
06-UJL-2000; 2000US-02154815P.
                                                                                                                                                                                                                                       LINSKE-O'CONNELL L I. WANG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 GGGCATGCATGGGGG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGCATGCATGGGGG 15
                                                                                                                                                                 ROBERDS S L.
BENJAMIN C W.
KARNOVSKY A M.
RUBLE C L.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-875311/81.
P-PSDB; ADE29295.
                                                                                                                                                                                                                                                                                  LIU D.
                                                                                                                                                                                                                     (RUBL/) H
(LINS/) I
(WANG/) W
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                                                                                                                                                                                       (BENJ/)
(KARN/)
                                                                                                                                                                   ROBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
8x3CCCCCCCCCCCCX8x111x2x3x111x2bbbbbbbbbxxxxxx
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; andiopolatin; apoptosis related protein; cacherin; cyclin; polymerase; oncogene, histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterflekin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; inflammation; nervous system disease; ss.
                                                                                                                               Human SNP oligonucleotide #4652.
1856 GGCATGCATGGGGG 1842
                                                               AAL31444 standard; DNA; 51 BP
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                           WO200147944-A2.
                                                                                                         24-JAN-2002
                                                                                                                                                                                                                                                                                                05-JUL-2001,
                                                                                    AAL31444;
                                         RESULT 5
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                                                                                                                    Gaps
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28-DEC-1999; 99US-0173419P. 27-DEC-2000; 2000US-00173419.

(CURA-) CURAGEN CORP

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                                                                                                                                                                                                                            9 9
                                                                                                                                                                                                                    Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                  Hou Y;
T, Zou G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 7; Length 2000;
Pred. No. 4.8e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2000 BP; 527 A; 468 C; 501 G; 503 T; 0 U; 1 Other;
                                                                                                                                    SA, Hou
Zhu T,
                                                                                                                                  Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 6147; 899pp; English.
                                                                                                  (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.6.
100.0%; Fre
                                                                                                                                  Cooper B,
                                  22-JUN-2001; 2001WO-IB001105
                                                                 22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGCATGCATGGGGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                  Chen W, Co
                                                                                                                                                                                     WPI; 2003-175290/17.
                                                                                                                                  Chang H, Che
Katagiri F,
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, appoiosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, interferons, interleukins, Gropoteins cytochromes, xinesins, cytokines, interferons, interleukins, Gropoteins cytochromes, xinesins, cytokines, interferons, interleukins, Gropoteins cytochromes, xinesins, cytokines, interferons, interleukins, Gropoteins cytochromes and thie peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes.

Systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukamai), diseases of the nervous system and an infection of pathogenic
                                                                                            Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 90.0%; Score 14.4; DB 4; Length 51; Local Similarity 93.8%; Pred. No. 7.8e+02; nes 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ovarian cancer related cDNA clone SEQ ID NO:1577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51 BP; 13 A; 7 C; 29 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1577; 489pp; English
                                                                                                                                                                            Claim 1; Page 2724; 4143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Algate PA, Harlocker SL, Jones R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2001; 2001WO-US017756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL78599 standard, cDNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207484P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCATGCATGGGGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 GGGCAGGCATGGGGGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                  Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-122075/16.
                                                           WPI; 2001-465210/50.
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                     Shimkets RA,
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Matches
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ABL78599
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The present invention describes a composition (I) comprising: carriers and almanostimulants, and a polypeptide (III) of a ovarian tumour polypeptide encoded by a polymucleotide (III) having a companient of Erom the 10912 nucleotide sequence (S2), a Teall population of (II), cor antigen presenting (II) having a sequence (S2), a Teall population of (II), cor antigen presenting cells that express (II). (I) has cycostatic activity. An oligomucleotide (IV) that bybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably cample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comprises contacting a biological cample from an exaction (FR). (I) comprising (III) and/or an expect the amount of polynucleotide hybridising to (IV) is detected preferably by calle and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme and protesins in tumour cells; and consequence a full length gene from a suitable library e.g., a tumour cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow transplantation and increasing platelet count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence codes for a derivative of human IL-3 having amino acids Arg, Leu, Leu and His at positions 64, 83, 88 and 99, respectively, subscituted by Lys, Pro, Met and Arg. The derivative has a higher activity than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 390 BP; 83 A; 144 C; 95 G; 64 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lys64, Pro83, Met88 Arg99 hIL-35 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 14.4; DB 6;
93.8%; Pred. No. 8.8e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                             library using well known techniques
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ID AAQ22507 standard; DNA; 408 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.8'
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIRI ) KIRIN BREWERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-120155/15.
P-PSDB; AAR22819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ22507;
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0; Gaps

Seguence 408 BP; 129 A; 105 C; 87 G; 87 T; 0 U; 0 Other;

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The 5' end of this strand overhangs the 3'end of the complementary strand by 4 bases; the 5' end of the complementary strand overhangs this strand by the terranuclatide sequence 5'-AATT-3'. The insert is used in the construction of plasmid pGGS8, which is in turn used in the construction of plasmids coding for human IL-3 derivs. See AAR22813-4, AAQ22503-Q22510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence codes for a derivative of human IL-3 having amino acids Arg, Leu and Leu at positions 64, 83 and 88, respectively, substituted by Lys, Pro and Met. The derivative has a higher activity than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
                                                                                                                                                                Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow transplantation and increasing platelet count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - for supplementing bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; interleukin-3; bone marrow transplant; graft; platelet;
hIL-34 derivative.
                                                                                                                                                                                                                                                                                                                                                       Query Match
90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                 Sequence 408 BP; 125 A; 104 C; 90 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human interleukin 3 deriv. and its prepn. - fo
transplantation and increasing platelet count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lys64, Pro83, Met88 hIL-3 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 21pp; Japanese.
                                                                                                                                                                                                         Example 1; Fig 19; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                             248 GGCCAGGCATGGGGGG 233
                                                       90JP-00279108
                                                                                  90JP-00087468
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGCATGCATGGGGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90JP-00279108
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AA<u>0</u>22506 standard; DNA; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KIRI ) KIRIN BREWERY
                                                                                                         (KIRI ) KIRIN BREWERY
                                                                                                                                       WPI; 1992-120155/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-120155/15.
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  JP04063595-A.
                                                                                                                                                                                                                                                                                                          and AAQ22513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1990;
                                                       19-OCT-1990;
                                                                                  03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow transplantation and increasing platelet count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence codes for a derivative of human IL-3 in which Arg, Leu, Leu, Thr, Ala, Thr, Ala and Phe at positions 64, 83, 88, 113, 122, 127, 132 and 134 have been substituted. The derivative has a higher activity than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                     K64, P83, M88, K113, E122, M127, B132, S134 hIL-3 coding sequence.
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                                                                                                                                                                                                                                                           Human; interleukin-3; bone marrow transplant; graft; platelet; hIL-36 derivative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin-3; bone marrow transplant; graft; platelet; sticky end; ds.
90.0%; Score 14.4; DB 2; Length 408; ilarity 93.8%; Pred. No. 8.8e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 14.4; DB 2; Length 408; 93.8%; Pred. No. 8.8e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert from plasmid pCGSB used to construct hIL-3 derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 408 BP; 133 A; 102 C; 86 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 8; 21pp; Japanese
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                                                                             246
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                                                                                                                                          :508/c
AAQ22508 standard; DNA; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ22510 standard; DNA; 408
                                                       1 GGGCATGCATGGGGG
                                                                                  261 GGGCAGGCATGGGGGG
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 93.8
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             (KIRI ) KIRIN BREWERY KK
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             Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR22820.
                                                                                                                                                                                                         04-SEP-1992
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                                                                                                                                                                              AAQ22508;
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  Query Match
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Matches
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Matches
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                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                           ss; sequencing by hybridisation; SBH; expressed sequence tag; BST; mapping; biodiversity; genetic disorder.
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones LW
                               90.0%; Score 14.4; DB 2; Length 408; ilarity 93.8%; Pred. No. 8.8e+02; Conservative 0; Mismatches 1; Indels
Sequence 408 BP; 130 A; 105 C; 86 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 462 BP; 89 A; 157 C; 141 G; 71 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   segdata.uspto.gov/seguence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 6563; 44pp; English.
                                                                                                                                                                                                                         ACH19351 standard; cDNA; 462 BP
                                                                                                                         261 GGCAGGCATGGGGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-2001; 2001US-00918995.
                                                                                                     1 GGGCATGCATGGGGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                              Human adult lung cDNA #354.
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LABAT I.
STACHE-CRAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615964/58.
                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                             13-OCT-2003
                                                                    15;
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                                                                                                                                                                                                                                                            ACH19351;
                                  Query Match
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LABA/)
STAC/)
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                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                   genome
                                                                    Matches
                                                                                                                                                                                                            ACH19351/
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Length 462;

90.0%; Score 14.4; DB 8; 93.8%; Pred. No. B.8e+02;

Query Match Best Local Similarity

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was ceteranized by the technique of SBH (sequencing by hybridisation). Also included is a purified polymeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences of are useful in diagnostics as expressed sequence tags (EST) for ceresponding to information of the novel polymucleotide. The nucleic acid sequences of corporation of the physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations of cereponsible for generic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of correcting antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                             ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 14.4; DB 8;
93.8%; Pred. No. 8.9e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stache-Crain B,
                                                                                                                                                                                                                            Human endothelial cell cDNA #1988.
                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00918995.
16
                                                                                                                      ACH33855 standard; cDNA; 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGCATGCATGGGGGG 16
                                                                                                                                                                                            13-OCT-2003 (first entry)
 1 GGGCATGCATGGGGGG
                                275 ecchicchicoboses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense DNA or RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-615964/58.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                          ACH33855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JONE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LABA/)
(STAC/)
(DICK/)
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                                                                                                                                                                                                                                                                                       genome
                                                                                     RESULT 12
                                                                                                          ACH33855/
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Sequence encoding gibbon ape leukemia virus-infected gibbon T-cell line UCD-144-MLA colony stimulating factor-80 (CSF-80).

AAN80502 standard; cDNA; 865 BP.

AAN80502/

(revised)
(first entry)

25-MAR-2003 06-DEC-1990

AAN80502;

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oni anaemia complementation group C; FAC; apoptosis; haematopoiesis; marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
                                                                                                                                                                                                                                                                                                                   New conjugate of Fanconi anaemia molecule and peptide selective for haematopoietic precursor cells - inhibits apoptosis of these cells, for treating Fanconi anaemia and patients undergoing high-dose chemotherapy
                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 48-49; 72pp; English.
                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                        AAV33946 standard; cDNA; 675 BP
340 GGGCAGCCATGGGGGG 325
                                                                                                                                                                                                                                           97US-0046546P.
                                                                                                                                                                                                                           98WO-US009975.
                                                                          (first entry)
                                                                                         Gibbon interleukin-3 cDNA
                                                                                                                                                                 1, .46B
/*tag=
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                                                                                                                                                                                                                                                                                                      P-PSDB; AAW68547
                                                                                                                           His-ILFAC; ds.
                                                                                                                                                                                                                                                                             Youssoufian H;
                                                                                                                                          Hylobates lar
                                                                                                                                                                                                                           15-MAY-1998;
                                                                          15-FEB-1999
                                                                                                                                                                                                                                           15-MAY-1997;
                                                                                                                                                                                           WO9851792-A1
                                                                                                                                                                                                                                                                                                                                               for cancer
                                                          AAV33946;
                                                                                                           Panconi
                                                                                                                    ропе
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This cDNA clone includes a coding region for gibbon interleukin-3 (IL3, see AAW68546). IL3 selectively binds to receptors on the surface of haematopoettic progenitor cells (HPC) and is transported into the cells by endocytosis. The invention provides conjugates, including fusion proteins, comprising human Fanconi anaemia complementation group C (FAC) protein (see AAW68546) and a targetting molecule such as gibbon IL3. These conjugates can be expressed e.g. in E. coli host cells utilising vectors encoding His-tagged IL3-FAC (termed His-ILFAC) fusions. The conjugate, or a mucleic acid encoding it, can be used to deliver FAC to an HPC, specifically to inhibit apoptosis, particularly in partients are exposed to high doses of chemotherapy for treatment of non-myeloid cancers, also to treat Fanconi anaemia (by complementation of the genetic defect). Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant production of conjugate in cell cultures) or in vivo. Treatment with FAC may eliminate the need for extensive bone marrow transplants to restore

Sequence 675 BP; 187 A; 192 C; 138 G; 158 T; 0 U; 0 Other;

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Gaps
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y Match 90.0%; Score 14.4; DB 2; Length 675; Local Similarity 93.8%; Pred. No. 9e+02; hes 15; Conservative 0; Misnatches 1; Indels C
                                                                                         1 GGGCATGCATGGGGGG 16
      Query Match
                                                   Matches
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324 GGGCAGGCATGGGGGG 309

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(revised)
(first entry)

25-MAR-2003 16-MAR-1990

AAN92339;

ö Non-coding portions may have a regulatory role in transcription in the natural host. The 3'-end contains an AT-rich segment including several repeats of the sequence ATTA, which is believed to be related to the RNA message stability. DNA sequence was used as a probe to obtain a 674EP DNA sequence from a human genomic library (AAN80503). (Updated on 25-MAR-2003 to correct PR field.) Primate IL-3 haematopoietic growth factors - used for treating disease states due to immune cell or haematopoietic cell deficiency. Gans Haematopoietic growth factor; lymphokine; interleukin-3; therapy; ö 90.0%; Score 14.4; DB 1; Length 865; 93.8%; Pred. No. 9.2e+02; Sequence 865 BP; 235 A; 224 C; 179 G; 227 T; 0 U; 0 Other; Indels /\*tag= a /product= "Leader secretory sequence" /\*tag= b /\*tag= b 0; Mismatches Location/Qualifiers Disclosure; ges 7-8; 51pp; English Yang YC; AAN92339 standard; DNA; 909 BP 86US-00885060. 86US-00893764. 86US-00916335. 87US-00021865. 349 GGGCAGGCATGGGGGG 334 1 GGGCATGCATGGGGGG 16 87WO-US001702. (GEMY ) GENETICS INST INC. Clark SC, Ciarletta AB, 15; Conservative WPI; 1988-036434/05. P-PSDB; AAP80502. Query Match Best Local Similarity diagnosis; es 06-AUG-1986; 07-OCT-1986; 04-MAR-1987; 13-JUL-1987; 14-JUL-1986; W08800598-A. mat\_peptide 28-JAN-1988 Gibbon. RESULT 15
AAN92339/C
1D AAN92
XX
AC AAN92
DT 25-MA
DT 16-MA Matches 8 셤

us-10-068-160-15.rng

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Fri Jul
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It is the nucleic acid sequence for maize locus 288. The tags indicate the location of primer sequences used in a rapid method of RFLP analysis. In the method each primer is labelled with a fluorescing molecule (chromophore) and hybridised with a restricted target DNA sample in the presence of an oligodeoxyribomucleotide elongating enzyme. Hybridisation is determined by reviewing the gels with a laser and appropriate detector no southern blotting is necessary. Tags A - B = primers 2388.

238A/238A3, 238AOLI, 238COLI and 238CI respectively. (Updated on 25-MAR-2003 to correct PR field.)
                                   Rapid RFLP analysis; chromophore; fluorescing molecule; maize loci 288; primers 238B, 238A/238AR, 238AOL1, 238COL1 and 238C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rapid restriction fragment polymorphism analysis, esp. in plant study using a primer labelled with a fluorescing molecule and an elongating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 909 BP; 196 A; 233 C; 244 G; 236 T; 0 U; 0 Other;
           Single stranded DNA sequence for maize locus 288.
                                                                                                                                                                                                                                                                                                                                                                                                                             Helentjaris TG, Lee MS, Shattuck-Bidens D;
                                                                                                       Location/Qualifiers 37. .57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 2 & 3; Page ?; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                        87US-00120309.
88US-00266970.
                                                                                                                                                                                                                                                                                                                               88BP-00310729
                                                                                                                                               / 103. .123

/*tag= b

305. .324

/*tag= c

636. .655

/*tag= d

882. .903

/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                  (NATI-) NATIVE PLANTS INC.
                                                                                                                                   /*tag=
                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                           13-NOV-1987;
03-NOV-1988;
                                                                                                                                                  misc_feature
                                                                                                                                                                              misc_feature
                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                             14-NOV-1988;
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0; Gaps

Query Match
90.0%; Score 14.4; DB 1; Length 909;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels (

Search completed: July 2, 2004, 08:31:35 Job time: 121.902 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

July 2, 2004, 08:09:30 ; Search time 25.0732 Seconds (without alignments) 354.132 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-068-160-15 16 1 gggcatgcatggggggg 16 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched: 1365418 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\*
1: /cgm2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgm2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgm2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgm2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgm2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgm2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 1689, Ap	Sequence 116, App	116,	116,	116,	116,	5, A	Sequence 5, Appli	54	107	285	m	Sequence 9, Appli	m,	1226	22,	30,	Sequence 454, App	17,	'n	ģ	Sequence 10, Appl	9	2	10,	10,
ID	US-09-252-991A-1689 US-08-807-342R-3	US-09-643-597-116	US-09-480-884A-116	- 1	US-09-606-421B-116	09-221-	09-266-	US-08-110-158-5	US-09-397-787-54	US-09-621-976-10744	US-09-252-991A-2852	US-09-180-109A-3	US-09-724-864-9	US-09-056-285A-3	09-023-	US-08-985-908-25	US-08-985-908-30	US-09-620-312D-454	US-08-026-138E-17	US-08-026-138E-5	US-08-026-138E-6	US-08-231-193A-10	US-08-486-273A-10	US-08-940-086A-10	US-08-940-035A-10	US-08-935-105A-10
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Score	14.4.	14.4	14.4	14.4	14.4	14.4	14.4	14.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4
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Sequence 10, Appl Sequence 10, Appl Sequence 9, Appli Sequence 1, Appli	Sequence 3, Applia Sequence 1, Applia Sequence 1, Applia Sequence 2996, Ap Sequence 659, App	Sequence 10, Appl Sequence 263, App Sequence 1580, Ap Sequence 264, App	Sequence 264, App Sequence 264, App Sequence 264, App Sequence 4088, Ap
US-09-648-797-10 US-09-386-123-10 US-08-436-332B-9 US-08-217-704C-1	US-09-754-250-3 US-09-539-333D-1 US-00-679-409-1 US-0B-956-171B-2996 US-09-328-352-659	US-08-480-474-10 US-09-025-769B-263 US-09-313-294A-1580 US-09-702-705-264 US-09-702-764	US-09-614-1248-264 US-09-671-325-264 US-09-589-184-264 US-09-489-039A-4088
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228 330 31	0 8 8 8 8 8 8 9 8 4 8 8 9	1000 1000 1000 1000 1000	0000 4444 8444 843 843 843 843 843 843 843 8

## ALIGNMENTS

KOLL HUMANOO
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 2, 2004, 07:38:45; Search time 1198.24 Seconds (without alignments) 398.746 Million cell updates/sec Run on:

US-10-068-160-15 Title: Perfect score: Sequence:

1 gggcatgcatgggggg 16

Scoring table:

27513289 segs, 14931090276 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST:\* Database :

em estba:\*
em esttum:\*
em esttum:\*
em esttun:\*
em estto::\*
em estto::\*
em estto::\*
gb\_est1::\*
gb\_est2::\*
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em gss\_tum:\*
em gss\_tum

Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	CB070440 tigr-ges-	AA808746 oe56h05.s	CB010201 Lb18G01 m	CB010108 Lb16E11 m
DI DI	CE070440	AA808746	CB010201	CROIDINA
æ	29	9	14	7
Length I	:			
Match	100.0	100.0	100.0	100.0
Score	36	16	16	36
No.	 	~	m	4
	Score Match Length DB ID	Score Match Length DB ID 16 100.0 178 29 CE070440	Score Match Length DB ID  16 100.0 178 29 CB070440  16 100.0 312 9 AA808746	Score Match Length DB ID 16 100.0 178 29 CE070440 16 100.0 312 9 AA808746 16 100.0 373 14 CE010201

AA798510 vx68f08.r AA798509 vx68f07.r B2317770 hx35a03.g B2308462 id42f07.b AL607489 Anopheles CE663190 tigr-ges- B2323566 ia79g11.g BH877725 hr54e02.g B2308895 id76f05.p	BZ371261 1e33b08.b BZ413880 if18e05.g BH881300 hv24f11.b AW044282 wv67all.x BZ966328 PUGGS75TD BZ994883 PUGGK75TB BZ374394 ie52406.g BZ416253 if65607.g	PUHRF48T if65cl0 if65cl1 bx347138 PUGBS95T PUFQSS9TI PUFQSS9TI Bx348859 Bx348859 Bx348859 Bx348859	BUSILE21 AGENCOURT AL52331 AL523331 BX356439 BX356439 AL200892 Tetracdon B1898692 480406 MA W23910 Zb47a07.r1 F22293 HEPD07000 H F22293 HEPD07000 H F20991 HEPD05425 H B1313004 daf89f08. AA406068 zu67b04.s AA496072 zu67b04.r
AA798 AA798 BZ31 BZ30 CNS0 CE66 BZ32 BZ320	BE2371266 BE41388 BE41388 BW044282 BE36632 BE396488 BB294488 BB294488	28 CC400096 28 BZ416255 28 BZ416245 13 BZ347138 29 CG129135 14 BZ348657 13 BZ371748 28 BZ792665 13 BZ371748 28 BZ792664 13 BZ3792664	3 ALG21512 3 ALG23531 3 ALG23531 3 CNSO4HG 2 M2189869 4 F22293 4 F22293 4 F22293 6 AA406068 AA406072
4 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	669 667 669 669 669 669 669 669 669 669	10099888444441 10099888844444 10099888884994	2011 1020 1020 1020 1020 1020 1020 1020
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### ALIGNMENTS

source

FEATURES

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/weeks.
/weeks
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10. ST 30-JUN-2003

LD16E11 mycelium of Laccaria bicolor grown for ten weeks Laccaria bicolor cDNA 5', mRNA sequence.
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Laccaria bicolor
Laccaria bicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Laccaria.
1 (bases i to 399)
Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D.,
                                                                                                                                                                                                                              Laccaria bicolor
Laccaria bicolor
Laccaria bicolor
Butaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Butaryota; Pungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
1 (bases 1 to 373)
Peter, M. Courty, P.-E., Kohler, A., Delaruelle, C., Martin, D.,
Pagu, D., Frey-Klett, P., Duplessis, S., Chalot, M., Podila, G. and
Martin, P.
Analysis of expressed sequence tags from the ectomycorrhizal
basidiomycetes Laccaria bicolor and Pisolithus microcarpus
Contact: Martin FM
Contact: Martin FM
CB010201

10.3 bp mRNA linear EST 30-JUN-2003

Lb16601 mycelium of Laccaria bicolor grown for ten weeks Laccaria
bicolor CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Laccaria bicolor"
/mol_type="mRNA"
/cultivar="6238N;
/db xref="taxon:22883"
/db xref="ten-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for ten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 16; DB 14; Length 373; 100.0%; Pred. No. 3.6e+03; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equipo de Microbiologie Forestiere
Equipo de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 69
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert Length: 37 Std Error: 0.00
Seq primer: Fornat 5' AAGGGGCCATTGGTTGGTACCC.
Location/Qualifiers
                                                                                                                                CB010201
CB010201.1 GI:32332827
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Matches 16; Conserv
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                         VERSION
KEYWORDS
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CB010108/c
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AUTHORS
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                                                                                                                                   ACCESSION
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/clone_lib="NCI_CGAP_Lubs"
/note="Organ: lung; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung; carcinoid, and was then primed with a not DECO RI adaptors (Pharmacia), digested with Not I and to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                     /mol_type="genomic DNA"
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/db_xref="taxon:9615"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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unknown library type
Insert Length: 413 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers

    .178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA808746.1 GI:2878152
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AA808746
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Best Local Similarity
Matches 16; Conserv
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tes 16; Conserv
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LOCUS

RESULT 2

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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Gaps

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Best Loc Matches

ORIGIN

RESULT 3 CB010201

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Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                    /sex="females"
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Matches 16; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepto,M., Tan,F., Underwood,K., Mooris,M., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:29883"
/dev_stage="ten-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for ten
Pagu, D., Frey-Klett, P., Duplessis, S., Chalot, M., Podila, G. and
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                       Martin, F.
Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes Laccaria bicolor and Pisolithus microcarpus New Phytol. 159 (1), 117-129 (2003) Contact: Martin PM
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The WashU-HMM Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                       Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert Length: 399 Std Bror: 0.00
Seq priner: Fornat 5' AAAGCCGCCATTGTGTTGGTACCC.
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Laccaria bicolor"
/mol type="mRNA"
/cultivar="S238N"
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AA798509 423 bp mRNA linear EST 10-FEB-1998 vx68f07.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1280389 5', mRNA sequence.
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Marral M., Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:672191
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This clone is available royalty-free through LLML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:672189
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WashJ-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108
Tel: 314 286 1800
Pax: 314 286 1810
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100.0%; Pred. No. 3.7e+03;
tive 0; Mismatches 0;
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                                                                                                                                            /organism="Mus musculus"
mol_type="miNA"
/mol_type="miNA"
/train="c57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:1280391"
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The WashU-HHMI Mouse EST Project
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/clone="IMAGE:1280389"
                                                                    Seq primer: -28ml3 rev1 ET fr
Location/Qualifiers
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Location/Qualifiers
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/strain="C57BL/6"
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GSS 06-NOV-2002

Query Match

ORIGIN

Best Loc Matches

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

LOCUS

RESULT 7 BZ317770

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High quality sequence stop: 525.

| Interest | Interest
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Anopheles gambiae GSS T7 end of clone 02L03 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
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Plate: id42 row: f column: 07
Seg primer: -21Ml3UnivFwd
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AL607489
AL607489.1 GI:15913674
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/tissue_type="whole skin"

/dev stage="11 weeks old"
/lab_host="$50# (kanamycin resistant)"
/lab_host="$50# (kanamycin resistant)"
/clone-lib="Stratagene mouse skin (#937313)"
/clone-lib="Stratagene mouse skin from 11 week old C57BL/6 female mice.
/clone-lib="Stratagene">female mice./female m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="fml07 or DH5a"

/lab_host="fml07 or DH5a"
/clone lib="WGS-Zmays" (JM.07 adapted methyl filtered)"
/clone lib="WGS-Zmays" (JM.07 adapted methyl filtered)"
/note="Grgan: immature ears: Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3: end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0:8 and 3 kb and were cloned into the vector (.x/y reads in MH3mpl9, .b/g reads in pUC19). The same ligation was transformed in either UM107 or DH5a. "
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S Rabinowicz, P.D., O'Shaughnesy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., C., Shaughnesy, A.L., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martiensen, R.S.,
Genomic shotgun sequences from Zea mays (methyl-filtered)
L. Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombie@cshl.org
Place: hx35 row: a column: 03
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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High quality sequence stop: 507.
Location/Qualifiers
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BZ317770.1 GI:24689877
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Best Local Similarity 100.
Matches 16; Conservative
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Zea mays
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db_xref="taxon:9615"
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Best Local Similarity 100.
Matches 16; Conservative
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Zea mays
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Matches
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VERSION
KEYWORDS
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ORGANISM
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BZ323566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
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                                                                                                                          Submitted (01-0CT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr 2 (bases 1 to 526)

Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

Submitted (01-0CT-2001) BBMI, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Carnivota; Pissipedia; Canidae; Canis. I (bases 1 to 511)
Rixhess; E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Praser, C.M. and
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 16; DB 29; Length 526; Local Similarity 100.0%; Pred. No. 3.9e+03; les 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NotreDamel"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7165"
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CE663190.1 GI:36982058
GSS.
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                                                                           Anopheles.
1 (bases 1 to 526)
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KEYWORDS
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                                                                                                            AUTHORS
TITLE
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AUTHORS
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PUBMED
                                                                                             REFERENCE
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JOURNAL
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   SOURCE
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/clone lib="WGS-ZnaysF (JM107 adapted methyl filtered]"
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The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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S Rabinowicz, P.D.; O'Shaughneesy, A.L.; Balija, V., Dedhia, N.;
Katzenburger, P.D.; O'Shaughneesy, A.L.; Balija, V., Dedhia, N.;
Katzenburger, P.; King, L.; Miller, B.; Muller, S.; Nascimento, L.;
Zutavern, T.; McCombie, W. R. and Mattiensen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Uppublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazen Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: iang row: g column: 11
Seq primer: -ZIMIJUnivRev
Class: shotgun
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/clone lib="Dog Library"
/note="Site i: BstXI; Libraries were prepared from
peripheral blood"
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                                                                                                                                                                100.0%; Score 16; DB 29;
100.0%; Pred. No. 3.9e+03;
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100.0%; Pred. No. 3.9e+03;
iive 0; Mismatches 0;
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Location/Qualifiers
1. .551
/organism="Zea mays"
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BZ323566.1 GI:24702199
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us-10-068-160-15.rst

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Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicooleae; Andropogoneae; Zea.

1 (bases 1 to 667)

2 Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Xatzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R., and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered)

L. Dupphilshed (2002)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874
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/lab_nost=".ydl07 or DH5a"
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/lone="Organ: immature ears: Site_1: XDa I; Site_2: XDa I;
The vector was digested with XbaI and one nucleoTide was added by fill in in the recessive 3; end. The genomic DNA was nabulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0:8 and 3 kb and ware cloned into the vector (.X/y reads in Milmpl9. b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
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1633b06.bl WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
BZ371261
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Gromic shotgun sequences from Zea mays (methyl-filtered) Grontact: W. Richard McCombie Lilta Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8874 Fax: 516 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
mol type="genomic DNA"
(CLLTivaz="BT3")
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/clone="id76f05"
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plate: ie33 row: b column: 08
Seq primer: -21Ml3UnivFwd
class: shotgun
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/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
re vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mpl9, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a.
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                                               ынв77725
hr54e02.gl WGS-ZmayBF (JM107 adapted methyl filtered) Zea mays
genomic clone hr54e02 5', genomic survey sequence.
BH877725
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Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Rabinowicz, P. D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Xatzebhurger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McComle, W.R. and Martienseen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

Pol Box 100, Cold Spring Harbor, NY 11724, USA

Fex: 516 367 8884
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Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N.,
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High quality sequence stop: 577.
Location/Qualifiers
1 577
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Plate: hr54 row: e column: 02
Seq primer: -21M13UnivFwd
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BH877725.1 GI:22113622
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Zea mays
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Search completed: July 2, 2004, 13:32:59 Job time : 1201.35 secs
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                                                                                                                             Query Match
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Matches 16; Conservative
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                                                                                                                                                                                          /clone="ie31000"
/lab host="This"
/lab host="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleoFide was
added by fill in in the recessive 3: end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (:X/y
reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DHSa."
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The vector was digested with XbsI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor lighated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y)
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reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."
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Gaps ô 100.0%; Score 16; DB 28; Length 673; 100.0%; Pred. No. 4.1e+03; ive 0; Mismatches 0; Indels

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68 GGCATGCATGGGGGG 83

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July 2, 2004, 08:11:05 ; Search time 123.317 Seconds (without alignments) 625.926 Million cell updates/sec
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19: /cgm2_6/prodata/2/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Description	Sequence 15, Appl	Sequence 119, App	Sequence 47, Appl	Sequence 47, Appl	Sequence 2017, Ap	Sequence 34086, A	Sequence 1577, Ap	Sequence 6563, Ap	Sequence 21067, A	Sequence 12515, A	Sequence 142400,	Sequence 142401,	Sequence 142400,	Semience 142401.
QI	US-10-068-160-15	US-10-194-035-119	US-09-802-668-47	US-10-243-475-47	US-10-087-192-2017	US-10-437-963-34086	US-09-867-701-1577	US-09-918-995-6563	US-09-918-995-21067	US-10-029-386-12515	US-10-027-632-142400	US-10-027-632-142401	US-10-027-632-142400	US-10-027-632-142401
	15	15	10	15	13	17	ወ	10	10	15	13	13	16	16
* Query Match Length DB	16	16	657	657	82660	388	390	462	475	518	607	607	607	607
& Query Match	100.0	100.0	93.8	93.8	93.8	90.0	90.0	0.06	90.0	90.0	90.0	90.0	90.0	90.0
Score	16	16	15	15	15	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	24.4
Result No.	rel	N	ო ს	Ω 4	S)	9	7	ω 00	O)	υ 10	11	12	13	14

RESULT 2 US-10-194-035-119

	90.0 691 16 US-10-027-632-283534 Sequence	90.0 822 13 US-10-027-632-157576 Sequenc	90.0 822 16 US-10-027-632-157576 Sequence	90.0 863 13 US-10-027-632-142398 Sequenc	90.0 863 13 US-10-027-632-142399 Sequenc	90.0 863 16 US-10-027-632-142398 Sequenc	90.0 863 16 US-10-027-632-142399 Sequenc	90.0 893 13 US-10-425-114-1734 Sequenc	90.0 959 16 US-10-282-596-94 Sequence	90.0 990 9 US-09-880-107-2366 Sequence	90.0 1616 13 US-10-027-632-257360 Sequence	90.0 1616 13 US-10-027-632-257361 Sequenc	90.0 1616 16 US-10-027-632-257360 Sequenc	90.0 1616 16 US-10-027-632-257361 Sequenc	90.0 1653 16 US-10-264-049-690 Sequenc	90.0 2001 15 US-10-240-965-243 Sequenc	90.0 2322 13 US-10-027-632-110914 Sequence	90.0 2322 16 US-10-027-632-110914 Sequenc	90.0 2529 9 US-09-969-708-575 Seguence 575	90.0 2529 13 US-10-240-425-1307	90.0 2529 13 US-10-342-887-485 Sequence 48	90.0 2529 13 US-10-172-118-485 Sequence 485,	90.0 2529 15 US-10-205-823-217 Sequence 217,	90.0 2529 16 US-10-236-031B-19 Sequence 19,	90.0 3079 9 US-09-735-705-116 Sequence 116,	90.0 3079 9 US-09-850-716A-116 Sequence 116,	90.0 3079 9 US-09-897-778-116 Sequence 116,	90.0 3079 10 US-09-466-396A-116 Seguence 116,	90.0 3079 13 US-10-007-700-116 Sequence 11	
14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	
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US-10-068-160-15

Sequence 15, Application US/10068160

Sequence 15, Application US/10068160

Sequence 15, Application World US/10068160

PUBLICANT: US20030066440A1

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: KINMAN, Dennis

APPLICANT: SECRETARY, Dennis

APPLICANT: USHIL, Ken

APPLICANT: VERTHELYI, Daniela

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

FILE REPERENCE: 4239-61999

CURRENT FILMS DATE: 1090-04-12

FRICK APPLICATION NUMBER: 60/128,898

PRIOR PILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LINGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Oligonucleotide US-10-068-160-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGCATGCATGGGGGG 16
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Query Match 93.8%; Score 15; DB 13; Length 82660; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2017, Application US/10087192
Publication No. US20020182586A1
FGENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
ITILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVELER: 2020-01-01
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: 2000-12-22
FRIOR APPLICATION NUMBER: 2000-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH E5660
      GENERAL INFORMATION:
APPLICANT: Roberds, Steven L.
APPLICANT: Benjamin, Christopher W.
APPLICANT: Benjamin, Christopher W.
TIVLE OF INVENTION: Human Ion Channels
TITLE OF INVENTION: Human Ion Channels
FILE REPERENCE: PHRM039-100
CURRENT APPLICATION NUMBER: US/10/243,475
CURRENT APPLICATION NUMBER: 60/403,254
PRIOR PLING DATE: 2003-01-16
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn version 3.2
SEGID NO 47
LENGTH: 657
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LCCATION: (1)...(82660)
CTHER INFORMATION: n = A,T,C or G
US-10-087-192-2017
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US-10-243-475-47
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US-10-437-963-34086/c
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US-10-087-192-2017/c
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Sequence 119, Application US/10194035

Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: FIRE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINGAN, Dennis
APPLICANT: KLINGAN, Dennis
APPLICANT: VERTHELYI, Daniela
APPLICANTON: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT APPLICATION NUMBER: US/00/101122
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR PILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SSOTHWARE PATENTIN VERT 2.11
SSO ID NO 119
LENGTH: 16
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100.0%; Score 16; DB 15; Length 16;
Best Local Similarity, 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 657;
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/09802668
Publication No. US20030190714A1
GENERAL INFORMATION:
APPLICANT: Wood, Linda
APPLICANT: Wood, Linda
APPLICANT: Lineke-O'Connell, Lisa I.
APPLICANT: Lineke-O'Connell, Lisa I.
APPLICANT: Lineke-O'Connell, Lisa I.
APPLICANT: Lineke-O'Connell, Lisa I.
APPLICANT: Line Berger 1000
TITLE OF INVENTION: Human Ion Charnels
FILE REPRENCE: 00069191
CURRENT PRILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,517
PRIOR PRILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PARENT VERIES AREHIT VERSION 3.0
SOFTWARE: PARENT VERSION 47
ILENGTH: 657
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
GENERALSM: Homo sapiens
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US-10-243-475-47/C
'Sequence 47, Application US/10243475
'Publication No. US20030194720A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 12515, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: HARLE, David R.
APPLICANT: HARLE, David R.
TITLE OF INVERTION: EXPRESSION ANALYSIS TWO
FILE REPERBACE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PLING DAVIE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12515
LIBRICH: 518
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21067, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyeeq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
| FILE REFERENCE: 2011-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT FILING DATE: 1999-01-20
| PRIOR FILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFTWARE: PRESENCE OF Windows Version 3.0
| SARO ID NO 21667
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.0%; Score 14.4; DB 10; Best Local Similarity 93.8%; Pred. No. 6.4e+02; Matches 15; Conservative 0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
TENGTH: 462
TYPE: DNA
PRATTRE:
PRATTRE:
                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: (1)...(462); OTHER INFORMATION: n = A,T,C or GUS-09-918-995-6563
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-918-995-21067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-918-995-21067/c
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US-10-029-386-12515/c
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                                                                              APPLICANT: Wi, Wei APPLICANT: Wi, Wei APPLICANT: Wi, Wei APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBYCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1577, Application US/09667701
Fatent No. USZO02013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
FAPLICANT: Gones, Robert
APPLICANT: Gones, Robert
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEG ID NOS: 10912
SOFTWARE: PASLESC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.0%; Score 14.4; DB 9; Length 390; Best Local Similarity 93.8%; Pred. No. 6.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Fublication No. US20030073623A1
Fublication No. US20030073623A1
GENERAL INPORMATION:
APPLICANT: Hyeaq, Inc.
TITLE OF INVANTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVANTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.0%; Score 14.4; DB 17;
Best Local Similarity 93.8%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38135C.1
US-10-437-963-34086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

LCCATION: (1)...(390)

CTHER INFORMATION: n = A,T,C or G

US-09-867-701-1577
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       Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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ORGANISM: Homo sapien
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US-09-867-701-1577
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) TYPE: DNA
) ORGANISM: Human
US-10-027-632-142400
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ORGANISM: Human
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US-10-027-612-142401
US-10-027-642-142401
Sequence 142401, Application US/10027632
Fublication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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                              OTHER INPORMATION: MAP TO CHR19.3
OTHER INPORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.5
OTHER INPORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
OTHER INPORMATION: EXPRESSED IN LING, SIGNAL = 4.9
OTHER INPORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
OTHER INPORMATION: SWISSPROT HIT: P09012; FVALUE 1.00e-09
OTHER INPORMATION: NT HIT: M60784.1, EVALUE 1.00e-09
OTHER INPORMATION: RST_HUMAN HIT: AW518377.1, EVALUE 1.00e-85
US-10-029-386-12515
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Publication No. US20020198371A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-027-632-142400
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Search completed: July 2, 2004, 13:58:24
Job time: 123.317 secs
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    US-1U-UZ-1-611442401, Application US/10027632;
Publication No. US20030204075A9;
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Mucleotide
TITLE OF INVENTION: Identification and Mapping of Single Mucleotide
TITLE OF INVENTION: David G.
TITLE OF INVENTION: David G.
TITLE OF INVENTION: DAVID: 108877.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
NUMBER OF SEQ ID NOS: 325720
SECOTA NO 142401
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LOCATION: (1) .: (617)

OTHER INFORMATION: unsure at all n locations

PEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_27843C.1

US-10-437-963-22690
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Publication No. US20040123343A1
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ORGANISM: Oryza Bativa
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US-10-027-632-142401
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US-10-027-632-142401
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LENGTH: 607
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Query Match 90.0%; Score 14.4; DB 17; Length 617; Best Local Similarity 93.8%; Pred. No. 6.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0.
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495 GGGCATGCACGGGGG 480

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	mcleic	search, using sw model
Run on:	July	2, 2004, 07:36:05 , Search time 633.732 Seconds (without alignments) 1231.080 Million cell updates/sec
Title: Perfect score: Sequence:	US-1 18 1 tg	-10-068-160-16 tgcgtcgatgcaggggggggggggggggggggggggggg
Scoring table:	IDEN	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272	272 segs, 21671516995 residues
Total number of	hits	Batisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: length:	h: 0 h: 200000000
Post-processing:		Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database .	_ 12643000000000000000000000000000000000000	
	339: 339: 41:	em_ntg_vr:* em_btgo_hum:* em_htgo_mus:* em_htgo_cther:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

CUMMAKIKS	Query Score Match Length DB ID Description		3 20 6 AX194440 AX194440	8 100.0 20 6 AXI94481 AXI94481	8 100.0 20 6 AX194482 AX194482	8 100.0 20 6 AX465390 AX465390	8 100.0 20 6 AX465431 AX465431	8 100.0 20 6 AX465432 AX465432	7 94.4 19 6 AX194483 AX194483	7 94.4 19 6 AX465433 AX465433	.4 91.1 18 6 AX352207 AX352207	.4 91.1 18 6 AX352217 AX352217	.4 91.1 18 6 AX352255 AX352255	.4 91.1 20 6 AX194432 AX194432	.4 91.1 20 6 AX194434 AX194434	.4 91.1 20 6 AX194437 AX194437	.4 91.1 20 6 AX194438 AX194438	.4 91.1 20 6 AX194439 AX194439	.4 91.1 20 6 AX194441 AX194441	.4 91.1 20 6 AX194443 AX194443	.4 91.1 20 6 AX194472 AX194472	.4 91.1 20 6 AX194502 AX194502	.4 91.1 20 6 AX352198 AX352198	.4 91.1 20 6 AX352201 AX352201	.4 91.1 20 6 AX352206	.4 JI.1 60 6 AASSEAUS ACC I I A AYRESSIS	4 01 1 00 6 axascons	4 91.1 20 6 AX352242 AX352242	.4 91.1 20 6 AX352245 AX352245	.4 91.1 20 6 AX352250	6.4 91.1 20 6 AX352254 AX352254	6.4 91.1 20 6 AX465382 AX465382	6.4 91.1 20 6 AX465384 AX465384	.4 91.1 20 6 AX465387 AX465387	.4 91.1 20 6 AX465388 AX465388	2 21.1 2 0 6 AVACCADA AVACCADA	.4 91.1 20 6 AX465393 AX465393	.4 91.1 20 6 AX465422 AX465422	.4 91.1 20 6 AX816067 AX816067	.4 91.1 22 6 AX352204	.4 91.1 22 6 AX352248 AX352248	.4 91.1 26 6 AX352228 AX352228 Sequenc	.4 91.1 26 6 AX352240 SAX352240 SAX352240 SAX352240 SAX352340 SAX352540 SAX352540 SAX352540 SAX525240 SAX525240 SAX525240 SAX525240 SAX525240 SAX525240 SAX5	16.4 91.1 28 6 AX35222 AX35222 Sequence		ALIGNMENTS			40 from Patent	AX194440 AX194440.1 GI:15385096		synthetic construct	synchetic constinct artificial sequences.	,	1, D., Ishii, K. and Verthelyi, D.	מייים מיי
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Vaccine against RSV
Patent: WO 0211761-A 58 14-FEB-2002;
HERRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Vaccine against RSV
Patent: WO 0211761-A 99 14-PEB-2002;
PERRY M. AACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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/mol xref="taxon:32630"
/note="Synthetic oligonucleotide"
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/db xref="taxon:32630"
/note="Synthetic oligonucleotide"
  Pred. No. 2.4e+02;
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 99 from Patent WO0211761.
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Sequence 58 from Patent W00211761.
AX465390
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AUTHORS
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AX465390
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Oligodeoxynucleotide and its use to induce an immune response
Parent: WO 0151500-A 82 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
1. 20
/organism="Synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151800-A 81 19-JUL-2001,
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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iive 0; Mismatches 0;
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
Location/Qualifiers
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/note="Synthetic DNA"

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    /organism="synthetic construct"
/mol_type="unassigned DNA"
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    /noCe="Synthetic DNA"

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RESULT 6 AX465432 LOCUS

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Mond,J.J., Prince,G. and Klinman,D.M.
Vaccine against RSV
Patent: WO 0211761-A 101 14-PEB-2002;
PRINT M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 503 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Fatent: WO 0193902-A 513 13-DEC-2001;
Biosynexus Incorporated (US)
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91.1%; Score 16.4; DB 6;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1;

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/noTe="Synthetic HDR"

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AX352207
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Oligodeoxynucleotide and its use to induce an immune response
Patent: NO 01515004 83 19-UU-2001;
Secretary of the pepartment of Health and Human Services (US)
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Vaccine against RSV
Patent: WO 0211761-A 100 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
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Sequence 100 from Patent W00211761.
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Sequence 83 from Patent WO0151500.
AX194483.1 GI:15385139
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Best Local Similarity 100.
Matches 17; Conservative
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PAT 28-AUG-2001
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Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 34 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Oligodeoxymuclectide and its use to induce an immune response Patent: NO 0151500-A 37 19-JUL-2001,
Secretary Of the Department of Health and Human Services (US)
Location/Qualifiers
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94.4%; Pred. No. 1.6e+03;
tive 0; Mismatches 1;
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/noTe="Synthetic DNA"
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Sequence 34 from Patent WO0151500.
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Sequence 37 from Patent WO0151500.
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                                                                                                                                    Query Match 91.1%; Score 16.4; DB 6; Length 18; Best Local Similarity 94.4%; Pred. No. 1.6e+03; Matches 17; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.6e+03;
0; Mismatches 1; Indels
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 551 13-DEC-2001;
Blosynexus Incorporated (US)
Location/Qualifiers
                1..18
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Sequence 551 from Patent WO0193902.
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Sequence 32 from Patent W00151500.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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linear PAT 28-AUG-2001
                                                                                                                                                                  Klinman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 38 19-JUL-2001;
Secretary of the Department of Health and Ruman Services (US)
Location/Qualifiers
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Sequence 38 from Patent WO0151500.
AX194438 AX194438.1 GI:15385094
                                                                                                    synthetic construct
synthetic construct
artificial sequences.
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Search completed: July 2, 2004, 10:08:03 Job time : 633.732 secs

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Query Match
91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels

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BQ102588 MINM172 M EX344896 BX448966 AV128107 AV128107 AA662789 1099369: S BB400545 AWB0C. GC CA706144 wdktc. pkc CA706144 wdktc. pkc CA70639337 wdm96.pkc AU001427 AU00142.7 CF639409 D15\_D01 F BL732664 BD15\_D01 F BL732664 BD15\_D01 F BL732664 BD15\_D01 F BL732664 BD15\_D01 F AV401323 AV401323 ACTOT792 COC671135 ACTOT792 COC671135 ACTOT792 COC671135 ACTOT792 COC671135 ACTOT792 COC77137 CC524815 CCTAR104 BH982312 CCHEN104 CC5254815 CCTAR104 CC5254815 CCTAR104 CC5254815 CCTAR104 CC62082 CCTAR104 CC62082 CCTAR105 BC74250 CCTAR104 CC62082 CCTAR104 CC62082 CCTAR104 CC62082 CCTAR104 CC62082 CCTAR104 BC920455 GC225447 CC62081 CCTAR164 BC920455 GC225445 BC920455 GC3244564 BC920455 GC3244678 BC920455 GC3444568 BC920455 GC3444678

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Sequence:

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CNSO9MAL
Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae tocal adult females. 3-PRIMS end of clone
FKOAAA28CA12 of strain 6-9 of Anopheles gambiae (African malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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Anopheles gambiae
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AV398286
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AV401323
BG707792
AU00123
BG707792
AU002103
AU0042213
BH982312
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CG254815
CG62082
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BX018781.1 GI:27568001
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CNSOBMNL
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BX018781 Single re
AA066330 mm14e06.r
BH746584 SALK 0448
AG082246 Pan Trogl
                                                                            2, 2004, 07:38:45; Search time 1348.02 Seconds (without alignments) 398.746 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                             27513289 Begs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
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AA066330
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AU173854 AU173854 BI758635 603027082 AV117227 AV117227 BZ579332 msh2\_6307

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Burvey sequence.
BH746584
BH746584.1 GI:18959699
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Best Local Similarity 94.4
Matches 17; Conservative
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/clone_lib="Stratagene muscle in initiation in its fire_l:
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/cloned tom diaphragm muscle in its fire_l:
/cloned unidirectionally from RNA
/clone size= 1.5 kb. Unit_AAP KR Vector; -5' adaptor
/cloneditionally fire managene in its fire_lib="Stratagene"
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/clo
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AA066330.1 GI:1563400
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Worris,M., Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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91.1%; Score 16.4; DB 9; Length 360;
Best Local Similarity 94.4%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels
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Trace considered overall poor quality
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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clone="FK0AAA28CA12"
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                            205 GCGTCGATGCAGGGGG 221
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                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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VERSION
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AUTHORS
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AA066330
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GSS 27-FEB-2002
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/clone="SALK 044872.30.00.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines ach of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 03-NOV-2001
                                                                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Mapolicophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 429)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shimn,P., Zimmerman,J. and Ecker,J.R.
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGOB2246 1110 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-079B07.R, genomic survey sequence.
AGOB2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
BH746584 SALK 044872.30.00.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atlg42480 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
111: 858 453 4100 x1752
Pax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/strain="Columbia 0"
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Gaps

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JOURNAL REPERENCE AUTHORS

TITLE JOURNAL

COMMENT

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893 bp mRNA linear EST 22-MAY-2003
EX448966 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
EX60DM012YN11 5-PRIME, mRNA sequence.
EX448966
EX448966.1 GI:31035980
EST.
                  /note="Vector: lambda Zap; Site_1: EcoRî; Site_2: Xhoî;, d-day.old mycella of Schizophyllum commune were transferred from minimal (nitrogen-replete) medium to fresh minimal medium. RNA was extracted twelve hours after
                                                                                                                                                                                                                                                                                                                                                                                                                    CB730492 17000315416995 Dog Library Canis familiaris genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (dog)
Canis familiaris
Canis familiaris
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
1 (bases 1 to 705)
1 (bases, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
clone_lib="MIN Nitrogen-replete Schizophyllum library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                          Length 489;
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                                                                                                                                                                        88.9%; Score 16; DB 13; I
100.0%; Pred. No. 9.9e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 16; DB 29; I
100.0%; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
                                                                                                           transfer and cDNAs prepared.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="Standard Poodle"
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1. .705
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CE730492.1 GI:37070612
                                                                                                                                                                                                                                                                                        143 CGTCGATGCAGGGGG 158
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Best Local Similarity 100.
Matches 16; Conservative
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14512627
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CE730492/c
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JOURNAL
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COMMENT
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DEFINITION
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Matches
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VERSION
KEYWORDS
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KEYWORDS
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           Totorians 1 to 1110)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Trumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gec.riken.go.jp, URL:http://hgp.gec.riken.go.jp/,
Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizophyllum commune
Schizophyllum commune
Schizophyllum commune
Schizophyllum commune
By Basidicanycota; Hyrenomycetes; Homobasidiomycetes;
By Basidiomycota; Hyrenomycetes; Homobasidiomycetes;
I (bases I to 489)
Jackson, E.N., Abner, A. Hittinger, C.T., Green, A.,
Lilly, W.W. and Gathman, A.C.
Bypressed sequence tags from Schizophyllum commune nitrogen-replete
Jupublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ102588 489 bp mRNA linear BST 12-APR-2002 MINM172 MIN Nitrogen-replete Schizophyllum library Schizophyllum commune cDNA 5' similar to stomatin, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contect: Gathman AC
Contect: Gathman AC
Biology Department
Southeast MO State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5735912361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 489
/organism="Schizophyllum commune"
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1110
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-079B07.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="4-40"
/db_xref="taxon:5334"
/tissue_type="mycelium"
                                                                                                                                                                                                                                                                                                                                                 Vector : pKS145
R.Site 1 : Saci
R.Site 2 : Saci
Location/Qualifiers
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Seg primer: T3
POLYA=No.
                                                                                                                                                                                                                                                                                                                                              : pKS145
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                                                                                                                                                                                                                                                                                                      Sequencing: M13Rev
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                 PRIMERS
                                                                                                                                                                                                                                                                                                                           LIBRARY
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LOCUS DEFINITION

RESULT 5 BQ102588

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

source

FEATURES

Gaps

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Gaps

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masyaoo, on NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:12-NOV-1997 masyaoo, on NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:1218808 3' similar to gb:X12794_cds1 V-ERBA RELATED PROTEIN EAR-2 (HUMAN);, AA662789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: GapDbs.rdmail.inh.gov

Email: GapDbs.rdmail.inh.gov

Email: GapDbs.rdmail.inh.gov

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/Libra at:

www-bio.llnl.gov/bbrp/image/image.html
trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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/tab host="DH108"
/clone lib="NCI CGAP Pr22"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pt7T3D-Pac (Pharmacia)
/note="Organ: prostate; Ist strand cNN was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 320) NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                            /sex="mixed"
/dev_stage="11-day embryo"
/clone_lib="Mus musculus C57BL/6J 11-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.1%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                               /organism="Mus musculus"
/mol type="mRNA"
/strain="CS7BL/6"
/db xref="taxon:10090"
/clone="2700054Bl5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1218808"
                                                                                                                                                                                 Location/Qualifiers
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Homo sapiens
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Unpublished (1997)
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AA662789/c
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Carninot, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Pukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Mori, F., Ishikawa, T., Itoh, M., Isawa, M., Kawai, J., Kihuchi, M., Kojima, Y., Matsuyama, T., Nitsuma, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganae, Y., Shibata, Y., Suzuki, H., Tateno, M., Tomaru, Y., Vokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., Mususe Ests

INDPUBLISHED (1999)

Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"

/organism="Homo sapiens"

/mol_type="mENA"

/downorses="texon:9606"

/clone="commonses="fexal"

/dow stage="fexal"

/dow stage="fexal"

/dow sapiens FETAL LIVER"

/note="Organ: liver; Vector: pCMVSPORT_6; lst strand cDNA

was primed with a NotI-cliqo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV slites of the pCMVSPORT 6

vector. Library was not normalized."
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Bax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY Cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, division of Invitrogen. Contact : Feng Liang Email :
fliang@lifetech.com URL : http://fulllength.invitrogen.com/
InvitroGen.Corporation 1600 Faxaday Avenue Genoscope sequence ID :
                                                      Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 893)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
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            sapiens (human)
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Best Local Similarity 93.84
Matches 15; Conservative
                                          Homo sapiens
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CA706144 42 bp mRNA linear BST 26-NOV-2002 wdklc.pk022.bl0 wdklc Triticum aestivum cDNA clone wdklc.pk022.bl0 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Peptratophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Dupont Wheat cDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
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/mol type="mRNA"
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/clone="wditc:ppe="kernel"
/clone="wdctor:pBluescript SK+; Wheat (Triticum aestivum
L.) developing kernel, 3 days after anthesis."
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Miao, G., Caraher, N. and Hanafey, M.K.
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
1 Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
1 Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
1 Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
1 Eax 302-631-2607

Email: Scott. V. Tingey@USA.dupont.com
Seq primer: M13.

Location/Qualifiers
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B. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Bmail: Scott.V.Tingey@USA.dupont.com
Seg primer: M13.
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Triticum aestivum
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1 (bases 1 to 366)

3 Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Close, T., Cloutier, P., Labocovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J. M., Jia, J., Oudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Shariflou, M., Sorrells, M., Warbutton, M. and Wenzel, G., Shariflou, M., Sorrells, M., Warbutton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

Unpublished (2000)

Contact: Langridge P. Species of the Triticeae
Unpublished (2000)

Contact: Langridge P. Species and Applied Plant Molecular Biology Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA Tel: 61 8 8303 7368

Fax: 61 8 8303 7308

Fax: 61 8 8303 7102

Fax: 61 8 8303 7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE400545
366 bp mRNA linear EST 21-JUL-2000
AWB004:G12F000328 ITEC AWB Wheat Melotic Stage Library Triticum
aestivum cDNA clone AWB004.G12, mRNA sequence.
BE400545
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/dev_stage="meiotic stage no later than metaphase I"
/dev_stage="meiotic stage no later than metaphase I"
/done lib="ITSC AMB Wheat Meiotic Stage Library"
/note="Wector: pSport I (life Technologies cat. no.
18248-013); Site I: Sall; Library constructed in pSport I.
Directionally cloned using the Superscript Plasmid System for DNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4
Kbp average insert size."
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ligated to Eco RI adaptors (Pharmacia), digested with Not I and Coned into the Not I and Eco RI sites of the modified prily vector. Library is normalized, and was constructed by Bento Soares and M. Fatina Bonaldo.
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                                                                                                                                                                     85.6%; Score 15.4; DB 9; Length 320;
larity 94.1%; Pred. No. 1.7e+04;
Conservative 0; Mismatches 1; Indels (
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/db_xref="taxon:4565"
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Ustilago maydis

Eukaryota; Puggi; Basidiomycota; Ustilaginomycetes;

Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

Is Usases I to 553;

S Nugent, K.G., Choffe, K. and Saville, B.J.

Gene Expression during Ustilago maydis Diploid Filamentous Growth:

EST Library Creation and Analyses

Unpublished (2003)

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3359 Mississanga Raad North, Mississauga, ON, L5L IC6, Canada

Tal: 905 569 4702

Fax: 
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Contact: Malbot V
Department of Biological Sciences
Stanford University
S55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 728 2227
Fax: 650 728 2227
Fax: 650 728 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
Sequence submitted separately.
Plate: 1008096 row: 26
Class: transposon-tagged.
1. .565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .553
|/organism="Ubtilago maydis"
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mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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1008096D04.x1 1008 - RescueMu Grid I Zea mays genomic, genomic
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AU001427 Bombyx mori b50(Dalzo) Bombyx mori cDNA clone fbm0407f,
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                                                                               Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Budopterygota; Lepidoptera; Glossata; Ditrysia;

Neoptera; Brochycidae; Bombyx.

E 1 (bases 1 to 499)
S Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.

Establishment of cDNA database of Bombyx mori
Unpublished (1999)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Rmail: Arthragenias.affrc.go.jp
PROJECT = 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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94.1%; Pred. No. 1.8e+04;
live 0; Mismatches 1;
                                                              organism="Triticum aestivum"
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        Location/Qualifiers
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CF639409.1 GI:37403984
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Matches 16; Conservative
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REFERENCE

PEATURES

ACCESSION VERSION KEYWORDS

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GSS 25-APR-2002

Fri Jul

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/organism="Zea mays"

/mol type="qenomic DNA"

/cullivar="mixed background W23/A188/B73"

/db xref="taxon:4577"

/tissue type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone lib="1008 - RescueMu Grid I"

/lab_host="Drgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BanHi; Site 2: BglII;

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BanHi; Site 2: BglII;

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BanHi; Site 2: BglII;

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScription on RescueMu; Group on RescueMu; Grot the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BanHI and BglII; and ligated to form circular plasmide. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Search completed: July 2, 2004, 13:33:02 Job time : 1351.14 secs

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0; Gaps

Query Match
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0;

ORIGIN

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(without alignments)
566.887 Million cell updates/sec
                                                                                                 2, 2004, 06:05:50 ; Search time 134.89 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                     3373863 segs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  - nucleic search, using sw model
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geneseqn1990s:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Immunogen Immunorea Immunorea CpG oligo CpG oligo CpG oligo CpG oligo D class C CpG D oli Immunogen Immunogen Immunorea Immunosti Immunosti Immunosti Immunosti Immunosti CpG D oli Immunorea Immunosti Immunosti Description Aac80620 Aa809531 Aa809530 Aa809530 Abk46510 Abk4650 Acc48298 Acc48319 Acc48319 Acc48319 Acc48319 Acc83124 | Add01050 | Aac80663 | Aa809633 Abk46511 Ab135587 Ab135577 Ab135625 Add01052 SUMMARIES AAS09590 AAS09632 ABK46510 ABK46468 ABK46509 ACC48312 ACC48312 ACC48306 ACC48319 ACC83117 ACC83124 ADD01050 AACB0661 AACB0620 AAS09631 AAS09633 ABK46511 ABL35577 ABL35625 ADD01052 ABL35587 염 % Query Match Length D 0.0001 100.0 0 8 Score 16.44 4.44 4.44 Result Š

Aac80619 Immunogen	Aac80621 Immunogen	Aac80652 Immunogen	Aac80614 Immunogen	Aac80612 Immunogen	Aac80617 Immunogen	Aac80618 Immunogen	Aac80623 Immunogen	Aas09622 Immunorea	Aas09591 Immunorea	Aas09582 Immunorea	Aas09587 Immunorea	Aas09589 Immunorea	Aas09593 Immunorea	Aas09584 Immunorea	Aas09652 Immunorea	Aas09588 Immunorea	Abl35576 Immunosti	Abl35582 Immunosti	Abl35586 Immunosti	Abl35568 Immunosti	Abl35624 Immunosti	
20 4 AAC80619	20 4 AACB0621	20 4 AACB0652	20 4 AACB0614	20 4 AACB0612	20 4 AACB0617	20 4 AACB0618	20 4 AACB0623	20 4 AAS09622	20 4 AAS09591	20 4 AAS09582	20 4 AAS09587	20 4 AAS09589	20 4 AAS09593	20 4 AAS09584	20 4 AAS09652	20 4 AAS09588	20 6 ABL35576	20 6 ABL35582	20 6 ABL35586	20 6 ABL35568	20 6 ABL35624	
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AAC80662 standard; DNA; 20 BP

AAC80662

AAC80662;

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Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent. CpG oligodeoxynucleotide, unmethylated, antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; natibody production; immune response induction; vaccine; allergy, asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple solenosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82. Verthelyi D; Claim 4; Page 36; 46pp; English. 12-APR-2000; 2000WO-US009839. 99US-0128898P. (first entry) D, Ishii K, (KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERI/) VERTHBLYI D. WPI; 2001-006880/01. WO200061151-A2. 12-APR-1999; 14-FEB-2001 19-OCT-2000. Synthetic. Klinman 

The invention relates to novel immunogenic CpG oligodeoxynucleotides

19-0CT-2000.

COMPATSON THE OLIGORUCLECTIES are at least 10 bases long and comparise one of the generic sequences 5'-NNWT-CpG-WNNA-3' or 5'-R'-CpG-RY - 3'. The central CpG morif is unmethylated, and the Oligonucleotides optionally have phosphorothhoate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery comprising an oligonucleotide of the invention and a targetting agent, and a pharmaceutcal composition comparising the oligonucleotide of the invention and a targetting agent, and a pharmaceutcal composition comprising the oligonucleotides are able to induce either a cell-nediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides are able to induce a humoral response. It is thought that after a cell-nediated response, and those of the sequence 5'-RNT-CpG-RNNN-3' being able to induce a humoral response. It is though that after administration, the oligonucleotide acts on antigen-presenting cells cadministration of natural killer (RN) cells. A cell-mediated or humoral response and dendritic cells), which then release cytokines, cleading to activation of natural killer (RN) cells. A cell-mediated or humoral response is useful for treating preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or of an inmunogenic CpG oligonucleotide is administered either alone or of incontination which may be treated include eczena, allergic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, laishmaina and schlatosomination infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, laishmaina and schlatosomination may also be erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency and symptome real maninger of an autoinmune disorder (e.g., lupus expense is lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention 

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Gaps ; reatch 100.0%; Score 18; DB 4; Length 20; Local Similarity 100.0%; Pred. No. 17; tes 18; Conservative 0; Mismarcher Query Match Matches

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1 TGCGTCGATGCAGGGGGG 18

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3 TGCGTCGATGCAGGGGG 20

AACB0661 standard; DNA; 20 BP AAC80661 

14-FBB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immuno response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protezzal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; bloological warfare agent; cytostatic; antiarthritic; antianterialergic; protezzacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothloate; ss.

Synthetic

WO200061151-A2.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AACEOSI-CeOTA). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences \$\frac{7}{3}\text{MNN}\$\text{ANN}\$ Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent. Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other; Verthelyi D; Claim 4; Page 36; 46pp; English 12-APR-2000; 2000WO-US009839. 99US-0128898P. Klinman D, Ishii K, (ISHI/) ISHII K. (VERT/) VERTHELYI D. WPI; 2001-005880/01. KLIN/) KLINMAN D. 12-APR-1999; 

Query Match 100.0%; Score 18; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 17; Matches 18; Conservative 0; Mismatches 0; Indels

0; Gaps

1 TGCGTCGATGCAGGGGG 18

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AAC80620 standard; DNA; 20 BP. AACB0620 ID AACB RESULT 3

AAC80620;

(first entry) 14-FEB-2001

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.

CpG oligodeoxynucleotide, unmethylated, antigen-presenting cell; immunogenic; cytokine release; natural killer cell; MK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; entibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; virtal; fungal; protezzoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; rimmune deficiency; biological warfare agent; cytostatic; antiarthritic; antiarthmatic; dermatological; phosphorothioate; se.

Synthetic.

WO200061151-A2

19-0CT-2000

12-APR-2000; 2000WO-US009839

99US-0128898P 12-APR-1999;

(KLIN/) KLINMAN D. (ISHI/) ISHII K. (VERT/) VERTHELYI D.

Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodecxymucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5.\*NNT-CpG-WANN-3. or 5.\*RY-CpG-RY CPG optionally have phosphorothicate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex. The invention also relates to an oligonucleotide delivery complex. The oligonucleotide of the invention and a targetting agent, and a phasmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cellmediated (T-cell) response or a humoral (B-cell, antibody) response, with colligonucleotides of the sequence 5.\*RNYT-CpG-WANN-3. The cellmediated response, and those of the sequence 5.\*NNYT-CpG-WANN-3. Desing able to induce a humoral response. It is thought that after administration, the oligonucleotide eacts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytchines, leading to activation of natural killer (WN) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably sathma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or the allergic conditions which may be treated include viral, the allergic conditions which may be treated include viral, and the infections which may be treated include viral, and a lateral creation (preferably sathma) or an infection of an autoimmune disorder (e.g., lupus conditions, and the infections which may be treated include viral, and in the treatment of an autoimmune disorder (e.g., lupus conditions, and the infections which may be an autoimmune disorder (e.g., lupus conditions, and the infections which may be an autoimmune disorder (e.g., lupus conditions, and the infections will and protocoal infections end and end of the treated

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immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to hymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CPG oligodeoxynucleotide of the invention
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0
                                                                                                                                           4; Length 20;
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                                                                                                        Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                           100.0%; Score 18; DB 100.0%; Pred. No. 17;
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                               1 TGCGTCGATGCAGGGGG 18
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Immunoreactive CpG sequence-containing oligonucleotide #81.

(first entry)

26-SEP-2001

AAS09631;

BP.

AAS09631 standard; DNA; 20

AAS0963

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; altergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; altergic ribinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HTV; malaria; Prancisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-442129/47.

Oligodeoxynuclectides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sednences 

Claim 5; Page 40; 48pp; English.

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences; where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or

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ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immundeficiency virus (HIV) and malaria, for treating immune system deficiency e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria
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Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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     4; Length 20;
                              0; Indels
     100.0%; Score 18; DB 100.0%; Pred. No. 17;
                              Mismatches
                            .;
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                                                       1 TGCGTCGATGCAGGGGGG 18
                                                                           TGCGTCGATGCAGGGGG 20
Query Match
Best Local Similarity 100.
Matches 18; Conservative
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RESULT

AAS09590 standard; DNA; 20 AAS09590 

(first entry) 26-SEP-2001

AAS09590;

Immunoreactive CpG sequence-containing oligonucleotide #40.

FN-gamma; humoral; antibody production; interleukin's production; therapoutic; allergy; asthma; cancer; autoimmune disorder; infection; blo-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; sequence; immune response; non-B cell activation; interferon gamma; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

40200151500-AL

12-JAN-2001; 2001WO-US001122

14-JAN-2000; 2000US-0176115P

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Verthelyi D; Ishii K, Klinman D,

WPI; 2001-442129/47

Oligodeoxynuclectides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG Claim 5; Page 33; 48pp; English. sednences

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell. mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleuklin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma,

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system e.g. autoimmune disorder or an immune system deficiency, infection of a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, uriticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines and other atopic conditions, for improving the efficacy of vaccines malaria, for treating immune system deficiencys, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, nubtriancial immunodeficiency syndrome (AIDS), Leistmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria
   e.g. solid tumour cancer, a disease associated
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Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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Gaps

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Gaps
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Score 18; DB 4; Length 20;
Pred. No. 17;
                         0; Indels
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 Query Match
Best Local Similarity 100.
Matches 18; Conservative
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AAS09632 standard; DNA; 20

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AAS09632;

(first entry) 26-SEP-2001 Immunoreactive CpG sequence-containing oligonucleotide #82

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfaze, vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistcosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1. 

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

ä Verthelyi Ishii K, Klinman D,

WPI; 2001-442129/47.

prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG Oligodeoxymucleotides for inducing an immune response to treat and sedneuces

Claim 5; Page 40; 48pp; English

AASO9551-AASO9662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The

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mediated immune response, involving non-B cell activation, interferon gamma (IRW-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune of system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is or used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhintis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines and other atopic conditions, for improving the efficacy of vaccines and other atopic maint eystem deficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, and atthrax and Listeria
are useful for inducing an immune response, preferably a cell
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100.0%; Score 18; DB 4; Length 20; 100.0%; Pred. No. 17; o; Mismatches 0; Indels Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other; 1 TGCGTCGATGCAGGGGGG 18 Local Similarity 100. Les 18; Conservative Query Match Matches δ

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Gaps

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ABK46510 standard; DNA; 20 RESULT 7
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ABR4 PARA
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ABRA PARA
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ABRA PARA
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ABRA PARA
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BP.

ABK46510;

05-JUN-2002

(first entry)

unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine; Paramyroviridea; F protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.

Immunostimulatory unmethylated CpG oligodideoxynucleotide #100.

Synthetic.

WO200211761-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US041633.

10-AUG-2000; 2000US-0224011P. 01-SEP-2000; 2000US-0229307P.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Klinman DM; Mond JJ, Prince G,

WPI; 2002-227118/28

epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.

The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by Quanthe linked by phosphate bond)-oligodideoxynucleotides (ODKs). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of

100.0%; Score 18; DB 6; Length 20;

Query Match

Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

vaccine

Claim 4; Page 9; 30pp; English.

The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodideoxynuclectides (ODNs). The

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           the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the creation of
 vaccine is useful for vaccinating a patient especially against viruses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                         unmethylated CpG; oligdideoxymucleotide; ODN; virucide; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramyxoviridae, F protein, respiratory syncytial virus; RSV, viral bronchiolitis, pneumonia, infectious pulmonary disease, bronchopulmonary dysplasia; congenital heart condition; ss.
                                                                                                                                                     6; Length 20;
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                                                                                                                                                                                                           1 TGCGTCGATGCAGGGGGG 18
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01-SEP-2000; 2000US-0229307P.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2002
                                                                                               the vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                       ABK46468;
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ABK46468
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CpG oligodeoxymucleotide, dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
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The method is useful for generating mature dendritic cells and enhancing response, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CpG oligodeoxymucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.
                                                                                 CpG oligodeoxynucleotide DV35 used for dendritic cell maturation.
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                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 8, 69pp; English.
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                                             (Eirst entry)
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Gursel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-300874/29.
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                                             11-AUG-2003
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      ACC48298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides.
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                   unmethylated CpG; oligdideoxymucleotide; ODN; virucide; vaccine;
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                                                                                                                                                                                                                                                                                                                            Immunostimulatory unmethylated CpG oligodideoxynucleotide #99.
                                                                                                                                                                                                                                                                                                                                                                                      Paramyxoviridae, F protein, respiratory syncytial virus, RSV, viral bronchiolitis, pneumonia, infectious pulmonary disease, bronchopulmonary dysplasia, congenital heart condition, ss.
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Pred. No. 17;
                         Indels
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    Pred. No. 17;
                         Mismatches
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                                                                                                                                                                                                      ABK46509 standard; DNA; 20 BP
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Best Local Similarity 100.0%;
Matches 18; Conservative 0;
100.0%;
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01-SEP-2000; 2000US-0229307P
                                                              1 TGCGTCGATGCAGGGGG
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                     18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prince G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-227118/28.
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mond JJ,
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                       Matches
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ABK46509
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Gaps

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Indels

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WC2003020884-A2.

13-MAR-2003

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ACC48298 standard; DNA; 20

RESULT 10 ACC48298

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RESULT 13
ACC48319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
                                                                                                                                    or as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                Generating mature dendritic cells for tumor immunotherapy or as va
for activating the immune system to treat diseases such as cancer,
comprises contacting a dendritic cell precursor with a D type
oligodeoxynucleotide.
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"N is any base (especially G) or no base"
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                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 7; Length 20; 100.0%; Pred. No. 17; o; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b
"N is any base (especially G)
                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                 Verthelyi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                            Disclosure, Fig 8; 69pp; English
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                                 14-AUG-2001; 2001US-0312190P.
          13-AUG-2002; 2002WO-US025732
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/note=
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                                                                                 Gursel M,
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                                                                                                         WPI; 2003-300874/29.
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Best Local Similarity
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misc_difference
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                                                                                DM,
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                                                                                 Klinman
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The present sequence is that of a D type CpG oligodeoxynucleotide that is an example of claimed D type oligodeoxynucleotides (see ACC48294) of the invention. Mature dendritic cells are obtained by contacting a dendritic cell precursor, such as a monocyte, with such an oligodeoxynucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infections or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell; tumour; immunotherapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of CpG oligodeoxynucleotide DV28 of the invention. A claimed method for generating dendritic cells involves
                                                                   Generating mature dendritic cells for tumor immunotherapy or as va
for activating the immune system to treat diseases such as cancer,
comprises contacting a dendritic cell precursor with a D type
oligodeoxymucleotide.
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cytostatic, immunostimulant, gene therapy, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
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Verthelyi D;
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                                                                                                                                                                                 Disclosure; Page 26; 69pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                produce activated T lymphocytes
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Best Local Similarity 100.
Matches 18; Conservative
Gursel M,
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                                   WPI; 2003-300874/29
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Klinman DM,
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contacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxymucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated T lymphocytes
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Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

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Gaps
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    Score 18; DB 7; Length 20; Pred. No. 17;
                       0: Indels
                        Mismatches
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Cuery Match
Best Local Similarity 100.0
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1 TGCGTCGATGCAGGGGGG 18 TGCGTCGATGCAGGGGGG 20

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ACC83117 standard; DNA; 20

(first entry)

27-AUG-2003

D class CpG ODN seguence useful for encapsulating in SSCL, DV28.

Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide; tuberculosis; cytokine; leishmaniasis; AlDS-associated Kaposi's tumour; thyroid; cancer; allargy: eczema; allargic rhinitis; coryza; hay fever; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; cps masthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis; CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; ss.

Unidentified

WO2003040308-A2.

15-MAY-2003

29-JUL-2002; 2002WO-US024235.

27-JUL-2001; 2001US-0308283P

25-JUL-2002; 2002US-00206407

IUSSH ) US DEPT HEALTH & HUMAN SERVICES.

Puri RK; Joshi BH, Ishii KJ, Kawakami K, Gursel I, Klinman DM,

WPI; 2003-482260/45.

Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.

Disclosure; Fig 10C; 110pp; English.

The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilishing agent and encapsulating a K type oligodeoxynucleotide (DDN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing interleukin-13 receptor in subject, for stimulating an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an in vivo or an in vitro immune cell, and for inducing an immune response against an in vitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxynucleotides including a CpG motif in clinical X4XEX8X**8**\$\$\$\$\$\$\$X8X8X8X8X8X8X8X8X8X8X8X8X8X8

The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilising agent and encapsulating a K type oligodeoxynucleotide (OWN) including a CpG motif. The invention is useful in pharmaceutical composition for impairing growth of a solid tumour cell (e.g. human tumour cell) bearing an interleukin-13 receptor in a subject; for stimulating an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunocherapeutic response against tumours or stimulating an in vivo or an in vitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxynucleotides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria,

Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide

Disclosure; Fig 10C; 110pp; English.

Kawakami X, Joshi BH, Puri RK;

Ishii KJ,

Klinman DM, Gursel I, WPI; 2003-482260/45.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxymucleotide; tuberculosis; grokine; leishmaniasis; AlDS-associated Kaposi's tumour; thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial; cysthma; utticaria; autoimmune disease; diabetes; rheumatoid arthritis; CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis; multiple sclerosis; infection; tumour; ss.
applications; for treating infectious diseases (e.g. tularemia, malaria, francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever, bronchial or allergic asthma, urticaria, food allergies), autoimmune diseases (e.g. diabetes, theumatoid arthritis, lupus erythematosus and multiple sclerosis) and psoriasis. The present sequence is a D class CpG ODN potentially useful for encapsulating in SSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D class CpG ODN sequence useful for encapsulating in SSCL, DV52.
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                                                                                                                                                                             'Match 100.0%; Score 18; DB 8; Length 20; Local Similarity 100.0%; Pred. No. 17; les 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                  1 TGCGTCGATGCAGGGGG 18
                                                                                                                                                                                                                                                                   3 TGCGTCGATGCAGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                  BP.
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25-JUL-2002; 2002US-00206407
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                                                                                                                                                                                  Query Match
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CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer CC bronchial or allergic asthma, urticaria, food allergies), autoimmune diseases (e.g. diabetes, rheumatoid arthritis, lugus erythematosus and CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
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Query Match
100.0%; Score 18; DB 8; iength 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: July 2, 2004, 08:31:35 Job time : 134.89 secs

3 TGCGTCGATGCAGGGGG 20

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Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appl
Sequence 1, Appli
Sequence 105, Appli
Sequence 105, Appli
Sequence 2, Appli
Ratent No. 5466585
Sequence 2941, Ap
Sequence 2941, Ap
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Sequence 1, Application US/09578441

Sequence 1, Application US/09578441

Sequence 1, Application US/09578441

GENERAL INFORMATION:
APPLICANT: Wu, J.H. David
APPLICANT: Omesa, Takeshi
APPLICANT: Chen, Yi-Guang
APPLICANT: Tsai, Ying-Chuech
TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2. ALPHA KINASE
FILE REFERENCE: 176/60571
CURRENT APPLICATION NUMBER: US/09/578,441
                   7681, Ap
1, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09799875

Sequence 16, Application US/09799875

Sequence 16, Application US/09799875

GENERAL INFORMATION:

APPLICANT: Meyers, Rachell

APPLICANT: Malliamson, Mark

TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses

TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses

TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses

TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses

TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses

FILE REPERENCE: 35800/20996

CURRENT PRILING DATE: 2000-03-06

FRIOR APPLICATION NUMBER: 60/182,059

FRIOR APPLICATION NUMBER: 60/182,059

FRIOR PILING DATE: 2000-09-12

FRIOR FILING DATE: 2000-09-12

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 2870

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               US-09-252-991A-7681
US-08-410-159-1
US-08-611-29-1
US-09-484-970B-66
US-09-484-970B-66
PCT-US91-09055-1
US-08-311-731A-1
US-09-131-731A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
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US-09-187-108-5
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NAME/KEY: CDS
LOCATION: (114)...(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-799-875-16
                                           Sequence 1455, Ap
Sequence 1425, Ap
Sequence 1425, Ap
Sequence 166, App
Sequence 6091, Ap
Sequence 6017, Ap
Sequence 6173, Ap
Sequence 6173, Ap
Sequence 55, Appl
Sequence 57, Appl
Sequence 7322, Ap
Sequence 7322, Ap
Sequence 7332, Ap
Sequence 7349, Ap
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Sequence 1, Appli
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Sequence 1, Appli
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Sequence 10, Appl
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Sequence 1, Appli
                                                                                                                                        July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds (without alignments) 354.132 Million cell updates/sec
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/ Gap2_6/ptodata/2/ina/5A_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/5B_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/6A_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/6B_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/6B_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/ Cgp2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-1486

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US-09-252-991A-6091

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US-09-252-991A-6091

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US-09-252-991A-6397

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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Perfect score:
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Maximum DB seq
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No.
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; TYPE: DNA

: ORGANISM: Mycobacterium tuberculosis

: OTHER INFORMATION: H37RV

US-09-103-840A-1
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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US-09-103-840A-1
iSequence 1, Application US/09103840A

Fatent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEICHMAN, Robert D.
APPLICANT: FLEICHMAN, Robert D.
APPLICANT: FLEICHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: SEQUENCE: 1998-06-24
NUMBER OF SEQUENCE: 1998-06-24
SOFTWARE: PALENTH VET: 2.1
SEQUENCE: BALCHIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: HITE, Owen R.
APPLICANT: HITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCLUGSIS
PILE REFERENCE: 24366-20007.00
CURRENT APPLICANTON NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                 Length 2891;
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                                                                                                                                                                                                                                                                                                 Score 14.4; DB 4;
Pred. No. 2.1e+02;
0; Mismatches 1;
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION UNMER: 60/135,713
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
LENGTH: 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      822321 CGTCGATGCAGGCGGG 822336
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Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           3 CGTCGATGCAGGGGG 18
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                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-578-441-ï
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RESULT 5

US-09-252-991A-1486/C

i Sequence 1486, Application US/09252991A

i Sequence 1486, Application US/09252991A

i Setent No. 6551795

i GENERAL INFORMATION:

A PELICANT: Marc J. Rubenfield et al.

A TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

I TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PELICATION NUMBER: US 60/074,788

PRIOR PELICATION NUMBER: US 60/094,190

PRIOR PELICATION NUMBER: US 60/094,190

PRIOR PELICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 759
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF TOTAGE 136
CURRENT PELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,786
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0;
Query Match

80.0%; Score 14.4; DB 3;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1;
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0;
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; Sequence 1592, Application US/09252991A
Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                              820143 CGTCGATGCAGGCGG 820158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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RESULT 10

US-09-252-991A-6091/C

Sequence 6091, Application US/09252991A

Returne 6091, Application US/09252991A

Returne 6091, Application US/09252991A

Returne 6091, Application US/09252991A

RETURNEY INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND ANID ANID THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

RETURNEY FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ERNOR FILING SATE: 1998-07-27

LENGTH: 552
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 4;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: Antisense Oligonucleotide
US-09-659-845A-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
FILE REFERENCE: RTS-0183
CURRENT APPLICATION NUMBER: US/09/659,845A
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 106
LENGTH: 20
TYPE: DNA
CURRENTS: ALLIficial Sequence
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6007
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Sequence 1690, Application US/09252991A
Sequence 1690, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABSUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 10796.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1690
LENGTH: 3591
                                                                                                                               US-09-252-991A-1425/c

Sequence 1425, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: APPLICATION NUMBER: US 60/074,738

PRIOR REPRENCE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,738

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1356
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; Sequence 106, Application US/09659845A
; Patent No. 6492170
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
APPLICANT: APPLICANT: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 4; Ler
Pred. No. 3.3e+02;
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ilarity 100.0%; Pi
Conservative 0;
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US-09-252-991A-1425
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US-09-252-991A-1690
       369 TGCGTCGATGCAGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       979 TGCGTCGATGCAGG 966
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Best Local Similarity
Matches 14; Conserv
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US-09-252-991A-1690
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us-10-068-160-16.rni

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GENERAL INPORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13 6
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WS-08-861-774E-55
; Sequence 55, Application US/08861774E
; Patent No. 629707
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Waters, Darbara
; APPLICANT: Ho. Yap
; APPLICANT: TONG, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BLOSYNTHESIS GENES FOR
; TITLE OF INVENTION: BLOACTIVE MOLECULES
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION UNBER: US/08/861,774E
; CURRENT PILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE PATENT OF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.7%; Score 13.8; DB 4; Length 642; Best Local Similarity 88.2%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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ORGANISM: Peltigera neopolydactyla
US-08-861-774E-55
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Best Local Similarity
Matches 15; Conserv
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; ORGANISM: Pseudi
US-09-252-991A-6014
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US-09-152-991A-6173/C
Sequence 6173, Application US/09252991A
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6173
LENGTH: 609
                                                                                                                                                                                                                                                                                          US-09-489-039A-7023/C
US-09-039A-7023/C
US-09-039A-7023/C
Sequence 7023. Application US/09489039A
Fatent No. 6610836
Patent No. 6610836
Patent No. 6610836
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7023
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   76.7%; Score 13.8; DB 4; Length 585;
88.2%; Pred. No. 4.1e+02;
tive 0; Mismatches 2; Indels
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US-09-252-991A-6173
                                                                                                                                                              TYPE: DNA
, ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7023
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                                                                                                                        2 GCGTCGATGCAGGGGG 18
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   Query Match
Best Local Similarity 88.23
Matches 15, Conservative
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RESULT 14 US-09-252-991A-6014/c ; Sequence 6014, Application US/09252991A

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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(without alignments) 625.926 Million cell updates/sec July 2, 2004, 08:11:05; Search time 138.732 Seconds 3163042 segs, 2412103800 residues - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 1 tgcgtcgatgcagggggg 18 US-10-068-160-16 18 Title: Perfect score: Sequence: Scoring table: OM nucleic Searched: Run on:

6326084 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
7	138	100.0	18	15	US-10-068-160-16	Segmence 16. April
7	18	100.0	20	5	US-10-068-160-7	
m	18	100.0	20	15	US-10-194-035-40	40.
4	18	100.0	20	15	US-10-194-035-81	Sequence 81. Appl
Ŋ	18	100.0	20	15	US-10-194-035-82	82,
ø	18	100.0	20	17	US-10-666-022-4	4
7	18	100.0	20	17	US-10-666-022-16	19
œ	17	94.4	19	15	US-10-194-035-83	83
σι	16.4	91.1	18	13	US-09-874-991C-503	503
O et	16.4	91.1	18	13	US-09-874-991C-513	513
ri	16.4	91.1	18	13	US-09-874-991C-551	
12	16.4	91.1	18	15	US-10-068-160-12	2
₽	16.4	91.1	18	15	US-10-068-160-14	4
14	16.4	91.1	18	15	US-10-068-160-18	Seguence 18, Appl

Sequence 20, Appl	494	497	502	505	e 508	e 512,	e 538,	541,	546	55	۲	26	31	38	Sequence 54, Appl	32	34,	37,	38,	39	41,	43,	7	H	H	Sequence 3, Appli	6	8	e 176,	Sequence 177, App
15 US-10-068-160-20	8-60-SD	Н	13	13 US-09-8	13 US-09-874-991C	13 US-09-874-9	13	13	П	13 US-09-874-9	15 US-10-068-1	~1	<del>,</del> 4	H	-	15 US-10-1	15	15 US-10-1	15 US-10-194~	Т	15	Н		15 US-10-194-035-102		US-10-666-02		US-10-666-02	-10-666-02	17 US-10-666-022-177
18	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	50	50	20	20	50	20	20	20	20
91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	٠,	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1
16.4	16.4	16.4	16.4	16.4	16.4	16.4	16 4,	16.4	16,4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	4.	43	4	<b>4</b> П

## ALIGNMENTS

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Sequence 16, Application US/10068160;
Publication No. US2030060440A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINRAN, Dennis
APPLICANT: KLINRAN, Dennis
APPLICANT: KLINRAN, Dennis
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE;
PILE REFERENCE: 4239-6199
CURRENT PILING DATE: 2002-02-06
PRIOR PILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIC DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SSOFTWARE: PATENTIC DATE: 1999-04-12
SSO ID NO 16
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide US-10-068-160-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 18; Conservative
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RESULT 2 US-10-068-160-7

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Sequence 82, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
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                       US20030144229A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
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US-10-666-022-4
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Matches
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Sequence 7, Application US/10068160

Publication No. US20030060440A1

GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SITINAMA, Dennis
APPLICANT: ISHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: USHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE REFERENCE: VOLGODBOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 2002-02-06
FILE REFERENCE: 2002-02-06
FRIOR APPLICATION NUMBER: US/10/068,160
FRIOR APPLICATION NUMBER: 60/128,898
FRIOR PRILICATION NUMBER: 60/128,898
FRIOR PRILICATION NUMBER: 09/24-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: CLINMAN, Dennis
APPLICANT: ISHLI, Ken
APPLICANT: USETHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT APPLICATION NUMBER: US/10/1122
PRIOR APPLICATION NUMBER: US/00/101122
PRIOR APPLICATION NUMBER: US/00/101122
PRIOR APPLICATION NUMBER: US/00/101123
PRIOR PEDPLICATION NUMBER: US/00/10113
PRIOR PEDPLICATION NUMBER: US/00/10113
PRIOR PEDPLICATION NUMBER: US/00/10114
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 40
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Oligonucleotide US-10-068-160-7
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Publication No. US20030144229A1
GENERAL INFORMATION:
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US-10-194-035-81
; Sequence B1, Application US/10194035
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ORGANISM: Artificial Sequence
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OP AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES.
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES.
APPLICANT: KINNAN, Dennis
APPLICANT: USHII, Ken
APPLICANT: VERTHELYI, Daniela
ITLEA OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT APPLICATION NUMBER: US/0/10/1122
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE PARENT PARENT OF SEQ ID NOS: 119
SEQ ID NO 81
LENGTH: 20
LENGTH: 20
LENGTH: 20
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APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KIINMAN, Dennis
APPLICANT: LISHI, Ken
APPLICANT: USHIL, Ken
APPLICANT: USHIL, Ken
CURRENT HILLOR DATE: 2002-07-12
FILE REFRENCE: 4239-6337
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT APPLICATION NUMBER: US/0/10/1122
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR PEDICATION NUMBER: US 60/176,115
PRIOR PEDICATION NUMBER: US 60/176,115
PRIOR PEDICATION NUMBER: US 60/176,115
SEQ ID NOS: 119
SEQ ID NO 82
LENGTH: 20
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ilarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches
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Sequence 83, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: SECRETARY OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE APPLICANT: VERTHELY, Dennis
APPLICANT: VERTHELY, Dennis
APPLICANT: VERTHELY, Daniela
TITLE OF INVENTION: OLIGOBOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2001-07-19
FRIOR PILING DATE: 2001-07-19
FRIOR PILING DATE: 2001-07-19
FRIOR PILING DATE: 2001-07-19
FRIOR PILING DATE: 2001-07-19
FRIOR APPLICATION NUMBER: US 60/176,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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Publication No. US20040652763A1
GENERAL INPORMATION:
APPLICANT: WORD, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: FLORA, MICHAEL
APPLICANT: TLINAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 503
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60;
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8-09-874-991C-513
Sequence 513, Application US/09874991C
Publication No. US20040052763A1
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Squence 16, Application US/10666022

GENERAL INFORMATION

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Realth and Human Services

APPLICANT: Secretary of the Department of Realth and Human Services

APPLICANT: Wetchelyi, Daniela

TITLE OF INVENTION: WETHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNCOMPROMISEL

TITLE OF INVENTION: SUBJECTS WITH INMUNOSTIMULATORY CPG

TITLE OF INVENTION WHERE: US/10/666,022

CURRENT APPLICATION NUMBER: US/10/666,022

CURRENT APPLICATION NUMBER: US 60/411,944

PRIOR APPLICATION WHERE: US 60/411,944

NUMBER OF SEQ ID NOS: 181

SOCTHARE: PatentIn version 3.1

SEQ ID NO 16

LEMOTH: 20
                                                GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services APPLICANT: Weithely', Daniela APPLICANT: Weithely', Daniela TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG TILL OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG TILL OF INVENTION NUMBER: US/10/666,022

CURRENT PILING DATE: 2002-09-17

PRIOR FILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 181

SEQ ID NO 4

LENGTH: 20
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LOCATION: (1)...(20)
POTHER INFRMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4
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Sequence 4, Application US/10666022
Publication No. US20040105872A1
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
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US-10-666-022-16
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GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: THE GOVERNMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: SHII, Ken
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI, Dennis
APPLICANT: VERTHELYI, Dennisla
APPLICANT: VERTHELYI, Dennisla
APPLICANT: VERTHELYI, Dennisla
APPLICANT: VERTHELYI, Dennisla
APPLICANT: VERTHERYIN, Dennisla
APPLICATION NUMBER: US,10,068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR PLILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: KLINMAN, Dennis
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REPRERENCE: 4239-6199
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT APPLICATION NUMBER: US/10/068,160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.1%; Score 16.4; DB 15;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1;
                                                                                                  FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin version 3:1
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide US-10-068-160-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/10068160
Publication No. US20030060440A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide US-10-068-160-14
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Publication No. US20030060440A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICANT: KINNMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: URTHELYI, Daniela
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR US-09-874-991C-551
APPLICANT: FLORA, MICHAEL

APPLICANT: FLORAN, MICHAEL

TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REPRENCE: 077797.0042-0

CURRENT APPLICATION NUMBER: U509/874,991C

CURRENT APPLICATION NUMBER: 60/209,797

PRIOR APPLICATION NUMBER: 60/209,797

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 620

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 513

LENGTH: 18
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Sequence 551, Application US/09874991C
GENERAL INPORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: MOND, JAMES J.
APPLICANT: FIGNA, MICHAEL
APPLICANT: KIINMAN, DENNIS M.
TITLE OF INVENTION: INMONOSTINULATORY RNA/DNA HYBRID MOLECULES
FILE REPRESENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SEQ ID NO 551
LENGTH: 18
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Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1;
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Sequence 12, Application US/10068160
Publication No. US20030060440A1
GENERAL INFORMATION:
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Best Local Similarity 94.4
Matches 17; Conservative
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US-09-874-991C-551
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RESULT 15
US-10-068-160-20
Sequence 20, Application US/10068160
Sequence 20, Application US/10068160
Sequence 20, Application No. US20030060440A1
GENERAL INFORMATION:
APPLICANT: THE COVERNERNT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: KLINRAN, Denniel
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: ISHII, Kan
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TILE REFERENCE: 4239-56199
CURRENT APPLICATION NUMBER: 60/128,898
PRIOR APPLICATION SEQUENCE: 120
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 18
TYPE: DNA
CREATER IN ATLIFICIAL Sequence
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PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 18
                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence PEATURE: OTHER INFORMATION: Oligonucleotide US-10-068-160-18
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Search completed: July 2, 2004, 13:58:25 Job time : 139.732 secs

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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetraodon nigroviridis pencine. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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      Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon
                                                                                                                                                                                                                                                                                                                                                                                                                             Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                  Roest Crollius.H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,?., Saurtin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
20256633

10835645
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AL183410.1
AL183410.1
GSS; genome survey sequence.
GSS; genome nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Actinopterygii, Telesostei; Buteleostomi;
Actinopterygii, Telesostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontoidea; Tetracdontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
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VERSION
KEYWORDS
SOURCE
ORGANISM
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PUBMED
REFERENCE
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TITLE
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CNS026IH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; I (bases 1 to 1417)

I (bases 1 to 1417)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-rémail.nih.gov

Tissue Procurement: DcTD/TP/Gazdar

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The 1.M.A.G.B. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at:

Hugh quality sequence start: 57

High quality sequence start: 57

High quality sequence start: 57

Location/Qualifiers
                                                                                                                                                                                                                          BU540484

1417 bp mRNA linear BST 13-SEP-2002
AGENCOURT_10325169 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6571942
5, mRNA sequence.
BU540484
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All66022.1 GI:7803760
GSs; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Tekracdon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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BST.
                                                       943 GCGCCGCCGCAGGGGG 959
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2 GCGCCGCCGCAGGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 17; Conservative
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ZMMBBD0343121.f ZMMBBb Zea mays subsp. mays genomic clone
ZMMBBD0343121 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays subsp. mays (maize)
Zea mays subsp. mays
Bukaryota, Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Dillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Lases 1 to 583)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
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                                                          Oryza sativa

Duyza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Poaceae; Shrhartoidaes; Oryzaae; Oryzaae; Oryzaa.

1 (Dases i to 57)

Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Partea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
B5721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 16.4; DB 14; Length 577; 94.4%; Pred. No. 4e+04; ive 0, Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                        1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="1 week"
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/note=F2-3 d 150mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4530"
/clone="0806F11-T3.abl"
/tissue_type="roots"
                                                                                                                                                                                                                                                                                                                                                                               Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1..577
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                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
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CG852075.1 GI:38378936
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    CA757679
CA757679.1 GI:25801718
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Best Local Similarity 94.4%;
Matches 17; Conservative
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BACKWARD: M13r
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Seg primer: T7
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CG852075
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BQ465952 660 bp . mRNA linear BST 30-MAY-2002 HT01C12T HT Hordeum vulgare subsp. vulgare cDNA clone HT01C12 5-FRYBE, mENA sequence. BQ465952. GI:21273734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="HT"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. bamHI, SalI,PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.
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Hordeum vulgare subsp. vulgare subsp. vulgare subsp. vulgare subsp. vulgare subsp. subsp. vulgare subsp. subsp.
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/db_xref="traxon:4578"
/clone="zwwwsbb0343121"
/lab_host="DH108"
/lab_host="DH108"
/clone=libe=zwwwsba"
/note="voctor: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stein Nils
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
Fax: 039482-5595
Fax: 039482-5595
Insert Length: 660 Std Brror: 0.00
Plate: 1 row: C column: 12
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/mol type="mRNA"
/cultivaz="barke"
/sub_goecies="vulgare"
/db_xref="taxon:112509"
/clone="HT01012"
/tissue_type="endosperm early"
/tissue_type="endosperm early"
/tab_host="X110-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barley BSTs from germinating seeds Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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BQ465952/c
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Class: BAC ends.
Location/Qualifiers
1. 583
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/mol\_type="genomic DNA"
/cultivar==873"

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us-10-068-160-17.rst

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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 676)
2 (bases 1 to 676)
2 (bases 1 to 676)
2 (bases 1 to 676)
                                                                                                                                                                                                                                                                                               Contact: Stein Nis
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 676 Std Error: 0.00
Plate: 1 row: N column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. 676
forganism="Hordeum vulgare subsp. vulgare"
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forultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo + scutellum"
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                                                                                                                                                                                                                                            Barley ESTs from germinating seeds Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Bub_species="vulgare"
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/clone="HS01ND3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, 2004, 13:33:05
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BQ466861.1 GI:21274643
EST.
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Job time: 1351.14 secs
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Xho1; mRNA was made from developing caryopsis (3.-15_DAP)
of spring barley variety 'Barke', a high quality malting
variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
(3'-end of cDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the RocoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp"
                                                                                                                                                                                                                                                                                                    EST 04-JAN-2001
(3.-15.DAP)
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Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (Dases; I to 671)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michaleköipk-gatrsleben.de, http://pgrc.ipk-gatersleben.de
Seg primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="XLOLR"
/clone lib="Hordeum vulgare Barke developing caryopsis
(3.-15.DAP)"
                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sub_species="vulgare"
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                                                                             0
                             Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 16.4; DB 9; Length 671; 94.4%; Pred. No. 4e+04; cive 0; Mismatches 1; Indels
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                          Score 16.4; DB 13; Length Pred. No. 4e+04; 0; Mismatches 1; Indels
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                                                                                                                                                                            498 TGCGCCGCCCCGGGGG 481
                                                                                                                             1 TGCGCCGGCGCAGGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                               AL508223.1 GI:12034438
                          Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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AL508223/c
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/dlone lib="MS"
/dlone lib="MS"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.1%; Score 16.4; DB 13; Length 676; Best Local Similarity 94.4%; Pred. No. 4e+04; Matches 17; Conservative 0; Mismatches 1; Indels 0;
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BQ466861 ST 30-MAY-2002 HS01N03T HS Hordeum vulgare subsp. vulgare cDNA clone HS01N03 S-PRIME, mENA sequence.

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531 TGCGCCGGCGCCGGGGG 514

RESULT 15 BQ466861/c LOCUS DEFINITION

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version - 2004	sw mode.	: 02:	18	1.0	16995	en par		)% Summaries		
GenCore (c) 1993	using s	07:36:05	-10-068-160-17 tgcgccggcgcagggggg	Gapext	21671516995	chos	00	0% 100% 45 su	*. ** N* * * * * ** O n n n n n n	in:* is:* iber:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

<u>.</u> .	Description	60 suid h	4 Gallus		AKU60251 Oryza sat	- 00	'n	12	64 Homo sa	64	4 0	ACL33/83 HOMO Bap1	0	Ŋ	6 Agrobact		AC018939 Homo sapi	_		. =	4	m	0 1	Axes4e33 sequence	212	Oryza	5 Oryza	30 Oryza	AKIU4655 UIYZA SAC axansassa sac	9 60	40 Oryza	38 Oryza	59 Tritic	96 Oryza	36 Oryza	O.sativa	94	NI.	99143	55179 Rattus	28
SUMMARIES	OI.	SHE5815			AK060251 AB01757881	AY422718	AB004065		AC10356										AC135854 SMR591784	PM3H12G					AX061421									AK0582	-	0514100		Α	MMMHB6	RNU55179	HSA132887
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# ALIGNMENTS

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Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, B.M.

Direct Submission

Binar-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

1 (Dases I to 232176)

Ghase, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                         Submitted (24-JUN-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics:
Sequencing vector: Plasmid, pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrasy version 0.990329.
**NOTE: This is a 'working draft' sequence. It currently
consists of I a contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1187 contig of 1187 bp in length
* 12635 12734; gap of unknown length
* 12635 12734; gap of unknown length
* 16457 16556; gap of unknown length
* 1657 26480; contig of 9224 bp in length
* 26580; 28999; contig of 1318 bp in length
* 26580; gap of unknown length
* 26580; gap of unknown length
* 26580; contig of 597 bp in length
* 26580; contig of 1318 bp in length
* 26590; contig of 587 bp in length
* 26590; contig of 587 bp in length
* 2650; contig of 587 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The order-orientation of the draft sequence was accomplished by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avid (http://baboon.math.berkeley.edu/mavid),
Lagan (http://lagan.stanford.edu/) and paired end information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=SREBF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Funding agent: Programs for Genomic Applications (NHLBI)
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Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                          Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERR
Center Project Name: G104
Bac Clone Name: CH261-22A23
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Direct Submission
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                                     Klupp.B.G.
Direct Submission
Submitted (27-AUG-2003) Klupp B.G., Institute of Molecular Biology,
FedResCen Virus Diseases of Animals, Boddenblick 5A, D-17493
Greifswald - Insel Riems, GERMANY
Location/Qualifiers
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Phasianinae, Gallus.
(Cases 1 to 232176)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="spaced direct imperfect repeats"
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/rpt_unit="156."183"
/rpt_unit="156."183"
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/rpt_type=INVERTED
/rpt_type=DIRECT
/rpt_type=DIRECT
/rpt_type=DIRECT
/rpt_unit="529."566"
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/note="inverted repeat of nt 442-523"
Trpt_type=InvERTED
166. .251
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product="ORF1.2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAE46335.1"
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1252. 31405
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HTG; HTGS PHASE2; HTGS DRAFT.
Gallus gallus (chicken)
Gallus gallus
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us-10-068-160-17.rge

FEATURES

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TICE.

WILL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagaahira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,W. Yamada,H., Doi,K., Kishimoto,N., Yazaki,T.,
Ishikawa,W. Yamada,H., Doi,K., Kishimoto,N., Yazaki,T.,
Shinamoto,M. and Nakahama,Y.
Isha Ganome Saquencing & Analysis Group: Ocomo,Y., Iida,Y.,
FAIS Genome Saquencing & Analysis Group: Ocomo,Y., Iida,Y.,
FAIS Genome Saquencing & Analysis Group: Ocomo,Y., Iida,Y.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsumoda,Y., Uu,M.,
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Genome Exploration Research Group in Riken Genomic Science Center
and Genome Science Laboratory in Riken: Adachi,J., Anzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fuyuda,S., Haranoto,K.,
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Takaku-Akahira,S., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S.,
Location/Qualifiers
Luce
           Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Yake, C., Yahdaj, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A. Collection, mapping, and annotation of 28K full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orysest PLN 24-JUL-2003
Orysa sativa (japonica cultivar-group) cDNA clone:001-004-C03, full
insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submission Shoshi Kikuchi, National Institute of Submitted (31-7M-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki S105-8602, Japan (E-mail:sKikuchi@niias.affrc.go.jp, Tal:81-29-838-7007, Fax:81-29-838-7007, Fax:81-29-838
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FLI_CDNA, oligo-capping.
Oryza sativa (japonica cultivar-group)
Gryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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Kikuchi,S.
                                                                                                                                                                                                                          from japonica rice
Unpublished
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TITLE
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AK060251/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sadachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Harashida, K., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashizaki, Y., Hayashida, R., Hida, Y., Haranto, K., Hiraoka, T., Hamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Karoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kibuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kodah, M., Koya, K., Kurihara, C., Kurosaki, T., Mikura, J., Miyazaki, M., Masuda, H., Matsupama, K., Murata, M., Nagata, T., Li, C., Lu, M., Nakamura, M., Namiki, T., Natsuyama, T., Murata, J., Mishi, K., Ooka, H., Ooka, H., Oasto, N., Ota, Y., Otomo, M., Ohtsuki, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Shinagawa, A., Shirataki, T., Sagah, Y., Suzuki, K., Satoh, K., Tagami, M., Sano, B., Takaku-Akahira, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK122136 616 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033135J16, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK122136.1 GI:37991782
EL_COMA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 94.4%; Score 17; DB 2; Length 232176; Local Similarity 100.0%; Pred. No. 1.4e+03; hes 17; Conservative 0; Mismatches 0; Indels 0.
11 232176: contig of 2796 bp in length. Cocation/Qualifiers
1. 232176
/organism="Gallus gallus"
/dol_type="genomic DNA"
/db_xref="texon:9031"
/clone="CH261-22A23"
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Science 301 (5631), 376-379 (2003)
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REFERENCE
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ACCESSION VERSION KEYWORDS

Пb

REPERENCE AUTHORS ö

Gaps

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AUTHORS

JOURNAL

TITLE

Length 616;

REFERBNCE AUTHORS

TITLE

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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Makamura,M., Nakamura,M., Nakamura,M., Namasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Tagama,T., Waki,K., Yasunishi,A., and Hayashizaki,Y.
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Best Local Similarity
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AB017578S1
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                                                                                                                                      Agrobiological Sciences Rice Full-Length cDNA Project Team.,
Kikuchi, S., Satoh K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J. Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobaysshi, W., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Miauno, K., Yokomizo, S., Mikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kasumedi, T., Coka, M., Kyu, R., Ueda, M., Matsubara, R., RIKRN:,
Kawai, J., Carninci, P., Adachi, J., Alaxawa, K., Rikra,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
Japonica rice
Libertian and Collection and
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Readchi J. Alzawa, K. Athmura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Fujimura, T., Pukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayashizaki, Y., Hayashida, K., Hiramoto, K., Haraoka, T., Inda, V., Iseda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishikawa, M., Itoh, M., Kagawa, I., Karapi, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Rurosaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, C., Rurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Nomura, K., Mizuno, K., Murata, M., Nagata, T., Nakamura, M., Namusaki, R., Oho, M., Ohtsuk, K., Satoh, K., Sakai, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pals Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fuls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulsosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Tsunoda,Y., Ueda,M., Ryu,R., Sugano,S., Sugiyama,A., Matsubara,K., and Murakami,K., Tsenode,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K., Adchi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hiraoka,T., Hori,F., Iida,J., Imamira,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagatta,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (05-DE20101) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-8602, Japan (E-mall:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                    The Rice Pull-Length cDNA Consortium, National Institute of
Shrhartoideae; Oryzeae; Oryza.
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AUTHORS
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cGMP-binding cGMP-specific phosphodiesterase; alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kotera, J., Fujishige, K., Imai, Y., Kawai, E., Michibata, H., Akatsuka, H., Yanaka, N. and Omori, K. Genomic origin and transcriptional regulation of two variants of cGMP-binding cGMP-specific phosphodiesterases

Eur. J. Biochem. 262 (3), 866-873 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (10-SEP-1998) Kenji Omori, Tanabe Seiyaku Co. Ltd.,
Discoverry Research Laboratory, Basic Technology Department; 2-50
Rawagishi-2-chome, Toda, Saitema 335-8505, Japan
(E-mail:k-omori@tanabe.co.jp, Tel:+81-48-433-8069,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2765. 72886
/product="cGMP-binding cGMP-specific phosphodiesterase"
/note="alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      groduct="cGMP-binding cGMP-specific phosphodiesterase"
note="alternative splicing
                                                                                                                                                                                                                                                                                      Gaps
iocation/Qualifiers
1.1665
7.0ganism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNya"
/cultivar="Nipponbare"
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/clone="001-004-C03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone_lib="EMBL3 SP6/T7 library (Clontech, USA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB017578S1 4225 bp DNA linear ROD 20 Rattus norvegicus gene for CGMP-binding cGMP-specific phosphodiesterase, exonla, exonlb and 5'-flanking region.
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                                                                                                                                                                                                                                     Length 1665;
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                  Score 16.4; DB 8;
Pred. No. 6.7e+03;
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/organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     1338 TGCGCCGGCGCAGGGAG 1321
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                                                                                                                                                                                                                                91.18;
                                                                                                                                                                                                                                                                                                                                       1 TGCGCCGGCCCAGGGGG
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                                                                                                                                                                                                                                                                                      17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MKQFLNFINGDFVATAKTFENRNPATNEVVGLVHEAGQAEVDAA
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WKVGPALACRQHQSSVKPSBETPATATLLGSVMMAVGHPKGSVPGAARLRPRIGRRIGRRIGRRIGRRI
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Purification, characterization, and gene analysis of catechol.
2,3-dioxygenase from the aniline-assimilating bacterium Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4247. . >4898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-MAY-1997) Shuichiro Murakami, Kobe University,
Department of Biofunctional Chemistry; 1-1 Rokkodai-cho, Nada-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-hydroxymuconic 6-senialdehyde dehydrogenase; catechol 2,3-dioxygenase; chloroplast-type ferredoxin; ORF3; ORF2; ORF1. Pseudomonas sp. Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami, S., Nakanishi, Y., Kodama, N., Takenaka, S., Shinke, R.
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Pred. No. 5.4e+03;
0; Mismatches 1; Indels 0;
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Biosci. Biotechnol. Biochem. 62 (4), 747-752 (1998)
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                                      db_xref="GI:37790595"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative (
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AB004065/c
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VERSION
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                                                                                                                                                                                                                                                                                                                          AY422718 4898 bp DNA linear BCT 26-OCT-2003 Pseudomonas sp. K82 catechol 2,3 gene cluster, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="WKLAHSLTVTAVSPQGSDAILLSLGVDGGQRQHFSFQSGQYLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. K82
Pseudomonas sp. K82
Bacteria; Potecobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,S.-I.
Direct Submission
Submitted (25-SEP-2003) Proteome Analysis, Korea Basic Science
Submitted (25-SEP-2003) Proteome Analysis, Korea Basic Science
Institute, 52, Yeoeun-Dong, Yusung-Ku, Daejon 305-806, Korea
Location/Qualifiers
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim,S.-I., Kim,J.-Y. and Kim,E.-A.
Proftcome analygis of aromatic compounds degrading bacterium,
Pseudonomas sp. K82
Unpublished
                                         ö
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels
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{trans1_table=11

{producf=aniline dioxygenase reductase"

protein_id=AAR03448_1"

db_xref="GI:37790593"
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| /codon start=1
| /transl table=11
| /product="putative Lys-R type regulator"
| /protein id="AAR034491"
| /db_xref="G1:37790594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pseudomonas sp. K82"
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/strain="K82"
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/codon start=1
/transl_table=11
/product="ferredoxin"
                                                                                                                                      3447 TGCGCCGCCGCAGGGGG 3464
                                                                                                1 TGCGCCGGCGCAGGGGG 18
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AY422718/c
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SOS

FEATURES COMMENT

SOS

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Direct Submission

Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Inumquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 2, 1998 this sequence version replaced gi:3550020.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Ems. EMBL; Sw: SWISSPROT; IT: TRENBL; WP: WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hann DNA linear FRI 05-JUN-2003
Human DNA sequence from clone RPS-117715 on chromosome 22g13.1
Contains a novel gene, the MSE55 gene for serum constituent protein
MSE55, the LGALS2 gene for soluble Galactose-binding Lectin 2
(Galactin 2, S-Lac Lectin 2, HJ14), ESTS, an STS, GSSS and two
putative CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                /evidenceeexperimental
/transl table=11
/product="2-hydroxymuconic 6-semialdehyde dehydrogenase"
/protein id="RAB18934.1"
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PRGAANPFKIFADIYGNVPTESPQMTTPDGGTAISYGLRTPLGVVGVICPWNLPLLLMT
WKVGPALACGNTVIVKPSEETLTLIHK"
                                 RMLQFKLPSGHEMRLYASKE FVGTDVGNINPDPWPDGLKGAGAHMLDHCLLMCEMNPE
AGINTVADNTRFMTEALDFFLTEQVLVGPBGNMQAATWMARTTTPHDIAFVGGPRSGL
HHIAFFLDSWHDVLKSADVMAKTXTRIDVAPTRHGITRGETIYPFDPSGNRNETFAGL
         WDEWDKYSVILTPSDQAGMMHLAYKVEKBADLEALQQKIEAWGVKTTMLDEGTLPSTG
                                                                                                                                                                                                                                                             'note="7 amino acids coded by Tn5 attached at C terminal."
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Mammalia; Butheria; Primates; Catarrhini; Fominidae; Homo.
1 (bases 1 to 96256)
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Pred. No. 5.3e+03;
0; Mismatches 1; Indels 0;
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HTG; CpG island; galectin; lctin; LGALS2; MSE55.
Homo sapiens (human)
                                                                                                                GYLAQRDRPVTTWT3DQLGSGIFYHTGYLVPSFTEVYT"
4245. .4808
/gene="alnG"
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/note="transposon Tn5-Mob"
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/gene="alnG"
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RFTLARHGQPVILYAGGSGIAPIFALRAREALLGGAPQWRLFYACRDRATAMILABIQA
LQAGSGQRLEIRHWYDAGGCPFYQALLBACYQGARADAYLCGBEARSVIAALBAA
GIEPGSYYREDPGAALGGAPTGAGPDABLTYQUKGGTHTVSVRGGPILGAMILDAG
LAVPHACRVGECASCMCRLVDGEVLRIDSSYLDBDDAABGWILLACRTRAASAQVRIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="GI:11610563"
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GNEWRARYSFTLABSREGHNRVLAGWNGFVLRQSAQGLVIVLKQVNLIDSDCLQGNNS
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TGAVAVQGYASRAYLARPHDYSASNPAPVDDHDILAMNLQFFHQDHNFTYANLDMAKF
GLIGKVRVQSDSFVPMALICALGHGYALLPKFVAADYPBLVPYPBKLFFFTELMLVSR
FDLLAAWQRELADRLQEEMATWPQ"
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fprotein id= Pahal8933.1"
db xref="GI:1610567"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MKLAHSLTVTAVSPQGSDAILLTLGVDGGQRQRFSPQSGQYLTL"
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db xref="GI:11610565"
'translation="MTRDGTTTPPWDLIRAFLALERHGSYEVAADMEGIDDSTLRRRI
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Kobe 657, Japan (B-mail:hakko2@kobe-u.ac.jp, Tel:81-78-803-0681,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'producE="chloroplast-type ferredoxin"
protein id="BAB18932.1"
'db_xref="GI:11610566"
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/gene="alnD"
2403. . 2678
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/function="electron transfer protein"
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                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/transl_table=11
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/evidence=not_experimental
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transl_table=11
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|db_xref="taxon:306"
                                                                                                                                            organism="Pseudomonas"
                        Fax:81-73-803-0680)
D86528:Submitted (08-Jul-1996).
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/gene="ainB"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction M13 subclone; and the assembly was confirmed by restriction migest, except on the rare occasion of the clone being a MAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/HGP/Chr22 constructed by the group of RP5-117715 is from the library RPCI-5 constructed by the group of http://www.chori.org/bacpac/home.htm
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707ct= 11.2 repeat: matches 2986. .3098 of consensus"

1294. .2310 mer AGCTACC 25% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 59. .299 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (#80. .554)
hote="MIR repeat: matches 186. .262 of consensus"
1092. .11102
hote="2.2 copies 5 mer CCTGG 22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copies 10 mer CTCCAGTGCT 35% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         020. .4132 -
note="MIR repeat: matches 60. .169 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .260. .1278
.note="19" O copies 1 mer G 29% conserved"
.1775
.note="MIR repeat: matches 29. .137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omplement (2493. .2617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            % 3174 motes. Matches 84. .191 of consensus. complement(3188. .3399) motes. MIR repeat: matches 36. .262 of consensus. notes. MIR repeat: matches 36. .262 of consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jace 239
2358 ...237
2358 ...237
2358 ...24 copies 9 mer TCTGCCAGC 44% conserved"
complement (2493. .2617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies B mer GGAGGAAG 36% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853. .2868 and conserved" note="2.3 copies 7 mer CCACCAT 23% conserved"
                                                                                                                                                                                                                                                                                                                              This sequence is the entire insert of clone RP5-117715.
Location/Qualifiers
1. .96256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copies 6 mer TCTCCC 37% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 .2334
note="2.8 copies 5 mer GTCAG 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900. .2911
note="2.4 copies 5 mer AGGC 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copies 5 mer CCTCT 27% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 copies 2 mer CT 51% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="5.0 copies 3 mer CCT 21% conserved" complement (4630. .4853)
                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="q13.1"
/clone="RP5-117715"
/clone_lib="RPCI-5"
1. .231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSq repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2735. .2755
/note="2.1 co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462. .3483
note="3.7 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466, .3483
note="3.6 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4270. .4284
/note="5.0 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494, .3523
note="15.0
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note="2.2 (
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/translation="DILEHDWREAQDSRQELCQXLHAVQGSLQWAESLRDQYLQ3MED
LRLKHRTLQKDCDLYKHRMATVLAQLESIEKERDQ"
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GCCCTGGTACCTGCTGCAGGCCCTCCTGACCACCCCCAG 526% conserved"
                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 2917. .3259 of consensus*
                                          copies 11 mer GGGCAGAGAGA 38% conserved"
                                                                                              consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MER5A repeat: matches 63, .163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Troce="MIR repeat: matches 43. .153 of consensus"
10759. .10750
Troce="L2 repeat: matches 3103. .3269 of consensus"
0863. .10882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="1.9 copies 11 mer CTGACCTGCCA 42% conserved"
11934. 11947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8067. .8176 ... Matches 49. .171 of consensus" Roce="MIR3 repeat: matches 49. .171 of consensus" 8742. .826. /note="2.4 copies 8 mer GCACACAG 29% conserved" 8365. .8386 /note="4.4 copies 5 mer CCAGC 26% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9358 .9652
forte="AluSx repeat: matches 1. .303 of consensus"
complement(join(10190. .10315,10888. .10998))
/gene="dJ117715.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                           7755. 8018
/note="AluSx repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8754. .8765
//notes="2"4 copies 5 mer GGGGA 24% conserved"
complement(8886. .9040)
/notes="MIR repeat: matches 13. .262 of consensus"
'note="MIR repeat: matches 16. .253 of consensus"
                                                                                                                                                                                                                               repeat: matches 81. .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1139. .11275
'note≈"MIR repeat: matches 70. .198 of consensusª
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (<10190. .10315, 10888. .>10998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/product==dully715.1 {PUTATIVE novel protein}"
/db_xref==qI:4808220"
                                                                                                                                      copies 6 mer CCCTCA 29% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 copies 6 mer CCCACA 21% conserved"
1611
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//note=12.0 copies 6 mer CCCATG 24% conserved"
//note=12.0 copies 6 mer GCCCTG 24% conserved"
                                                                                                                                                                                   copies 5 mer CCTCA 25% conserved"
                                                                                                                                                                                                                                                                               copies 5 mer GAGGG 24% conserved"
                                                                                                                                                                                                                                                                                                             7140. .7157
/note="3.6 copies 5 mer GGAGA 29% conserved"
complement(7185. .7506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0053. .11082
.0045=#4.0 copies 5 mer GGGCA 31% conserved"
.054. .11064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="2.2 copies 5 mer CAGGG 22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="2.5 copies 4 mer GGAA 20% conserved" 1139. .11275
                                                    5878. .5895

7,000 = "L2 repeat: matches 3003. .3060 of 5878. .5895
                                                                                                                                                                                                                                                                                                                                                                                                    .637. .7650
'note="14.0 copies 1 mer A 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="supported by predicted exons
match: ESTs: Em:AA316883"
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/note="MIR re
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note="15.6 cc
         /note="2 F
                                                                                                                                                            5879. .5895
/note="3.4 c
                                                                                                                                                                                                                                                           7058. ,7069
/note="2.4 c
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Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 15, 2002 this sequence version replaced gi:18677687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-FBB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 106117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S VanBrunt, A., Kozlowicz, A. and Spalding, L.

VanBrunt, A., Kozlowicz, A. and Spalding, L.

The Sequence of Homo sapiens BAC clone RP11-788A1

Unpublished (26 Homo sapiens BAC clone RP11-788A1

3 (bases 1 to 106117)

5 Waterston, R.H.

L Submitted (28-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Loum MO 63108, USA

8 (bases 1 to 106117)

S Waterston, R.H.
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Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MD 63108, USA
6 (bases 1 to 106117)
                                                                                                                                                                                     /note="AluSx repeat: matches 1. .308 of consensus"
13480. .13747
/note="AluJb repeat: matches 30. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC103564 106117 bp DNA linear PRI 23-M
Homo sapiens BAC clone RP11-78BA1 from 2, complete sequence.
AC103564
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                                                                                                                                                                                                                                                                                                                                            Length 96256;
12557. .12569
/note==2.2 copies 6 mer GCCCTG 26% conserved."
/note==5.8 copies 6 mer CTCCTT 70% conserved*
12763. .12775
/note==2.2 copies 6 mer TTGAGC 26% conserved*
13154. .13468
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 9;
Pred. No. 2.9e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulston, J.B. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGCGCCGCCCAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC103564.5 GI:19482407
                                                                                                                                                                                                                                                                                                                                      Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (human)
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Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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AUTHORS
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JOURNAL
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AC103564
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Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens EST AI651841 (NID:94735820)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphisms exist between AC103564, AC093724 and AJ239322. Data from AC093724 was used to finish AC103564.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the right is AJ239322, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-788A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. Mopping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MCD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted:
Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                    Center project name: H_NH0788A01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="RPCI-11"
548. 568
/rpt family="AT_rich"
659. 1023
/note="similar to Homo s:
wb50e02.x1"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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2451 .2767
/rpt family="BRV1"
2772 .2914
/rpt family="L1"
2915 .3208
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/rpt_family="Alu"
1743. .2012
/rpt_family="Alu"
2213. .2320
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/rpt_family="MIR"
954. .960
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Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nippombare(GA3) genomic DNA, chromosome 8, BAC clone:OSJNBa0049G15
L Published Only in Database (2002)
E Published Only in Database (2002)
S Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
Submitted (11-APR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Oapan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On May 21, 2003 this sequence version replaced gi:20142142.
The orientation of the sequence is from -21M13 to M13rev of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
BAC clone:OSJNBa0049G15, complete sequence.
AP005064
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Homo sapiens BAC clone RP11-1L5 from 2, complete sequence.
AC093724 AC012122
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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| 15599 | 15932 | 1599 | 1599 | 1599 | 1599 | 1599 | 1599 | 1599 | 1599 | 1599 | 16267 | 16267 | 16269 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 1659 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 | 17168 |
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| forganism="Oryza sativa | faponica cultivar-group} |
| fullivar="Nipponbare" |
| fullivar="Nipponbare" |
| fullivar="Nipponbare" |
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Pred. No. 2.8e+03;
0; Mismatches 1; Indels 0;
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91.1%; Score 16.4; DB 9;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1;
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Best Local Similarity 94.4%;
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AP005064/c
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SOURCE
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AC093724
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14474. 14586
14474. 14586
157bf_family="ERV1"
15168. 15423
/rpt_family="Alu"
15168. 15188
/note="similar to Homo sapiens EST BF062548
(NID:g10821458)"
15168. 15180
/note="similar to Homo sapiens EST AA211483 (NID:g1810137)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1237. .11247
note="similar to Homo sapiens BST AA453375 (NID:g2167044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match to EST BG221911 (NID:g13747932)"
5245. .6660
'rpt family="MaiR"
:661. .7534
5377. .8028
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0255. 10562
00000="match to EST BG221911 (NID:g13747932)"
0284. 10707
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aote="match to EST BG221795
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12642. 12753
12762. 12753
12762. 13191
/rpt family="(TA)n"
13193. 13473
13528. 13556
                                                                                                                                                                                                                                                                                                                                                         977. .6763
note="match to EST
031. .6813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /537, .8028
/rpt_family="ERV1"
8037. .831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6037. .8331
/rpt_family="Alu"
8359. .8990
/rpt_family="MalR"
8993. .938
                                                                                                                /rpt_family="L1"
5153. .5365
/rpt_family="BRV1"
                                                                                                                                                                                                                                                      rpt_family="ERV1"
536. .5999
rpt_family="ERV1"
577 675
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rpt family="Malk"
3006. .10226
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rpt_family="ERV1"
1766. .11949
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4116, .14329
rpt_family="BRV1"
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2574. .12641
rpt_family="Alu'
209. .3921
                                                          'rpt_family="L1"
1396. .5149
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the clone

ORGANISM

VERSION KEYWORDS SOURCE

AUTHORS TITLS JOURNAL

REFERENCE

MEDLINE

PUBMED REFERENCE AUTHORS TITLE JOURNAL

AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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This sequence is the entire insert of the clone. This clone is overlapped by AC093838 and AC103564.
                                                                                                               The sequence of AC012122 has been incorporated into AC093724.
Location/Qualifiers
1. .161617
                                                                         Bacterial transposon in unfinished region of
                                                                                                                                                                                        /organism="Homo sapiens"
| mol_type="genomic DNA"
| db_xref="taxon:9606"
| chronosome="2"
| map="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394. .8622
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122. .9278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="MSR2_type"
937_.8029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15239. .15296
'rpt_family="AT_rich"
6597. .1688?
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich"
2193. .2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="(TAGA)n"
1891. .12048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="AT_rich"
5239. .15296
                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-11"
1894. _1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="ERV1"
5187. .6400
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6401. .6421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="ERV1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MaiR"
0031. .10316
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|rpt_family="Alu"
|078. .5130
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1309. .11415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt family="MIR"
2119. .12402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="Alu"
2403. .12561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt family="MIR"
2930. .12950
                                                                                                                                                                                                                                                                                                                  'clone="RP11-1L5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt family="Alu"
261. .3382
                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
2828. .3125
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1383. .3783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="L1"
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3394, .8622
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2587. .12833
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2 (bases 1 to 161617)
2 (bases 1 to 161617)
The sequence of Homo sapiens BAC clone RP11-1L5
Unpublished (2001)
3 (bases 1 to 161617)
Waterston, R.H.
Direct Submission
University School of Medicine, 4444 Porest Park Parkway, St. Louis, Meterston, R.S.
H. (10-SEP-2001)
We have set 1 to 161617)
We have set 1 to 161617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (30-MAY-2003) Department of Genetics, Washington
Submitted (30-MAY-2003) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 30, 2003 this sequence version replaced gi:19033950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MRA-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5. (bases 1 to 161617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                             Enkaryogica, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

( Dases 1 to 161617)

Sulston, J. E. and Wilson, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0001L05
Drafting Center: WIBR
          AC093724.3 GI:31194053
                                                       Homo sapiens (human)
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                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.
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NEIGHBORING SEQUENCE INFORMATION:

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Submitted (18-SEP-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                                                                                                              1114: contig of 1114 bp in length 1214: gap of unknown length 2766: contig of 1552 bp in length 4107: contig of 1241 bp in length 4207: gap of unknown length 5500: gap of unknown length 5500: gap of unknown length
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contig of 1148 bp in length
gap of unknown length
contig of 1286 bp in length
gap of unknown length
contig of 1752 bp in length
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contig of 3141 bp in length
gap of unknown length
contig of 7383 bp in length
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 1 (bases 1 to 182944)
Materston, R.H.
The sequence of Homo sapiens clone Unpublished
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                                                                 2 (bases 1 to 182944)
Waterston, R.H.
Direct Submission
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1215
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4208
5401
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68881
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                                                                                                                                                                  COMMENT
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HTG; HTGS_PHASE1.
HTmo sapiens (human)
Homo sapiens sapiens (human)
Human)
Human sapiens (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.6e+03;
0; Mismatches 1; Indels 0;
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39197, 39231
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'99460, 39380
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28857. .28898
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4. .39978
family="AT_rich"
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family="AT_rich"
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. .37800
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19402. .39420
                                                                                                                                                             7804. .27820
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rpt_family="Mariner"
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34554. .34724
/rpt_family="MIR"
35381. .35728
                                                                                                                                                                                                                                                                                                                                                                                             family="(T)n"
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rpt_family="L2"
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family="L2"
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23547. .23688
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Best Local Similarity 94.4%;
Matches 17; Conservative
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AC133783/c
LOCUS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny D. Marzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Aoyagi, A., Bada, E., Bada, M., Benahmed, F., Balan, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bardar, M., Barnstead, M., Benahmed, F., Bardar, J., Blair, J., Blarber, M., Barnstead, M., Benahmed, F., Cavazos, I., Ceasar, H., Center, A., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, E., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, G., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermon, C., Dinh, H., Divya, K., Draper, H., Duya, S., Dumn, A., Durbin, X., Duval, B., Baves, K., Bedand, C., Cockrell, R., Gener, C.A., Falls, T., Foster, P., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratus, P., Haaland, W., Hanli, C., Hamilton, C., Hamilton, K., Harnandez, S., Haddun, S.L., Hodgson, A., Hounel, J., Jackson, A., Jackson, A., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Karpathy, S., Kelly, S., Khan, Z., Xing, L., Kovar, C., Karpathy, S., Kelly, S., Khan, Z., Xing, L., Kovar, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC133256 235115 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-198G22, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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91.1%; Score 16.4; DB 2; Length 182944;
Best Local Similarity 94.4%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC133256.2 GI:25139160
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULITOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                          note="assembly_name:Contig32"
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4208. .5400
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AC133256/c
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Lorenanhear, M. Walter, C.L., Laboow, H. Lavan, J. Lewis, L. Liz, Liu, J., Lorenanhear, L. Loulsoged, M. Older, S. L. Marker, L. L. M. Mannoul, M. Malter, M. Martin, E. Monten, M. Martin, E. Monten, M. Martin, M. M
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Assembly program: Phrap; version 0.990329
Consensus quality: 208631 bases at least Q40
Consensus quality: 208631 bases at least Q30
Consensus quality: 210832 bases at least Q20
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Center code: BCM
Web site: http://www.hgsc.bcm.tec.edu/
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Center project name: GYYD
Center clone name: CH230-517B22
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Direct Submission
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AUTHORS
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AUTHORS
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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91.1%; Score 16.4; DB 2; Length 235115;
Best Local Similarity 94.4%; Pred. No. 2.46+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                        232090 232189; sopt of 232089 bp in length 232090 232189; sape of unknown length 2332190 233481: contrig of 1292 bp in length 233882 23518: contrig of unknown length 233582 235115: contrig of 1534 bp in length. Location/Qualifiers
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AC121480/c
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvlak, P., Hawes, A., Henderson, N., Hernandez, M., Hines, S., Hiladun, S.L., Hodgson, A., Hogues, M., Garnandez, M., Hines, S., Hiladun, S.L., Hodgson, A., Hogues, M., Jacob, L., Jang, H., Johnson, B., Johnson, R., Lovar, C., Liu, J., Liu, J., Liu, J., Liu, J., Lovan, J., Levan, J., Lewis, L., Liu, J., Lovan, M., Mahindarine, M., Mahindarine, M., Mahindarine, M., Martinez, B., Moncens, R., Margua, P., Martinez, B., Moncens, R., Mangum, R., Mangua, P., Martin, R., Martinez, B., Moncens, R., Morgan, M., Morris, K., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, R., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, R., Morris, S., Mortemayor, J., Morris, R., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, R., Morris, S., Mortemayor, J., Moore, S., Morgan, M., Morris, R., Morris, S., Mortemayor, J., Parks, K., Pasternak, S., Paul, H., Perez, L., Peraz, L., Peraz, L., Peraz, R., Pal, S., Parks, R., Pals, R
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23907725.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the Eature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....- Genome Center
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                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                              FEATURES
                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.ngsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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ans str. C58 circular chromosome, section 60
    Estimated insert size: 211250; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens CS8
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
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Agrobacterium tumefaciens str. C58 (Cereon)
Bacteria; Proteobacteria; Alphagroteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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91.1%; Score 16.4; DB 2; Length 235785;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                      1 91766: contig of 91766 bp in length 57 91866: gap of unknown length 57 106790: contig of 14924 bp in length 91 106890: gap of unknown length 91 235785: contig of 128895 bp in length. Location/Qualifiers
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of 254 of the complete sequence.
AE008002 AE007869
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91867
106791
106891
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AE008002/c
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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transl_table=
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GAPRITEDGYSVAKEIELEDKFENMGAQLYNEVYSKTHDIAGDGTTTATVTAQLIVE

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COMDLEMENT (7253. . . 7549)

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complement (3903. .4394)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="AGR C 1226"
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Pseudomonas aeruginosa (strain PA01)"
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gene

SCO

gene

CDS

gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.9%; Score 16; DB 1; Length 10029; 100.0%; Pred. No. 6.8e+03; Live 0; Mismatches 0; Indels 0
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Job time : 637.732 secs
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8825, or
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Best Local Similarity
Trans 16; Conserva
                                                                                                                                                                                                                              gene
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gene

SOS

CDS

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
              Copyright
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OM nucleic - nucleic search, using sw model

Run on:

July 2, 2004, 06:05:50; Search time 134.89 Seconds (without alignments) 566.887 Million cell updates/sec

US-10-068-160-17 18 Perfect score:

1 tgcgccggcgcagggggg 18 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s:\*
genesequ290s:\*
genesequ200s:\*
genesequ2001as:\*
genesequ2001bs:\*
genesequ2002s:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* N Geneseq 29Jan04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	ACC48302 And of the	Aa110608	Aa117683	Aac41286	Aaa79481		AAC56198 Aac56198 Eucalyptu	ABI99675 Mouse		ACA42729 Prokaryot					•	Abv21138		ABV29359 Human	ABV25524 Human	ABV28091 Abv28091 Human	ABV28883 Human	ABV22253	
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di	Query Match	100.0	85.6	85.6	85.6	92.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6		85.6	85.6	85.6	85.6	85.6	'n.	85.6	85.6	85.6	
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Abv24860 Human pro	Abv25159 Human pro	Abv23047 Human pro	Abv23269 Human pro	Abv25226 Human pro	Abv28062 Human pro	Abv29113 Human pro	Abv25353 Human pro	Ada53342 Human cod	Aad09560 Human tra	Aak69788 Human imm	Aak98307 Human pro		Aak98309 Human pro	Aak98317 Human pro	Aak98311 Human pro	Aak98306 Human pro		Aak98315 Human pro	Aak98314 Fuman pro	Fuman	
ABV24860	ABV25159	ABV23047	ABV23269	ABV25226	ABV28062	ABV29113	ABV25353	ADA53342	AAD09560	AAK69788	AAK98307	AAK98308	AAK98309	AAK98317	AAK98311	AAK98306	AAK98316	AAK98315	AAK98314	AAK98313	AAK98318
2929 5	2929 5	2929 5							-				3918 6			3918 6				3918 6	 
85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	ď.			'n.	'n.	85.6	'n
15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	H5.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
C 24	O 53	c 36	N	c 28	?	'n	'n	32	33	34	c 35	c 36	c 37	ი 38	c 33	c 40	C 43	O 42	o 43	O 44	Ω 45

## ALIGNMENTS

CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss. /\*tag= a /note= "N is any base (especially G) or no base" CpG oligodeoxynucleotide used for dendritic cell maturation. Location/Qualifiers ACC48302 standard; DNA; 20 BP. (first entry) Key misc\_difference misc\_difference 11-AUG-2003 Synthetic. ACC48302; RESULT 1 ACC48302 

/\*tag= b /note= "N is any base (especially G) or no base"

WO2003020884-A2.

13-MAR-2003.

13-AUG-2002; 2002WO-US025732.

14-AUG-2001; 2001US-0312190P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Gursel M, Verthelyi D; Klinman DM,

WPI; 2003-300874/29.

Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.

Disclosure, Page 26; 69pp, English.

The present sequence is that of a D type CpG oligodeoxynucleotide that is an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

ó

Gabs

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Indels

<del>.</del>

Mismatches

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Conservative
       16;
                                                                                                                                                                                                                                                                                 19-JUL-2001
                                                                                                                                     AAL17683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
       Matches
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invention. Mature dendritic cells are obtained by contacting a dendritic cell precursor, such as a monocyte, with such an oligodeoxymucleotide. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, manitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                          Score 18; DB 7; Length 20;
Pred. No. 2.3e+02;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 374 BP; 69 A; 109 C; 122 G; 68 T; 0 U; 6 Other;
                                                                                                                       Sequence 20 BP; 1 A; 5 C; 11 G; 1 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                  Human breast cancer expressed polynucleotide 3065.
                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 4;
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 569; 3695pp; English.
                                                                                                                                                                                                                                                      RESULT 2
AAL10608/c
ID AAL10608 standard; cDNA; 374 BP.
                                                                                                                                                                     0;
                                                                                                                                                                                            1 TGCGCCGGCGCAGGGGGG 18
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                                                                                                                                                        ilarity 100.0%;
Conservative
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2000US-0205230P.
2000US-0211315P.
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94.1%;
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                                                                                                                                                          Local Similarity
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15-MAY-2000; 2
09-JUN-2000; 2
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                                                                                                                                               Query Match
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Matches
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to human breast cancer expressed polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 450 BP; 83 A; 138 C; 146 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Human breast cancer expressed polynucleotide 10140.
                                                                                                                                                                                                                                                                                                                                                               cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                AAL17683 standard; cDNA; 450 BP
                                              288
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18
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2000US-0205230P.
2000US-0211315P.
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2000US-0192099P
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25-JUL-2000; 2000US-0220534P
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1D AAC41286 standard; DNA; 499
XX
AC AAC41286;
XX 17-OCT-2000 (first entry)
                                              304 GCGCCGCCGCATGGGGG
2 GCGCCGCCGCAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GCGCCGGCGCAGGGGG
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Les 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200151628-A2.
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990S-0139817P.
990S-0140383P.
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990S-0140283P.
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990S-014332P.
990S-0144332P.
990S-0145088P.
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990S-014508P.
990S-0147322P.
990S-0149308P.
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990S-0149308P.
  22 - JUN - 1999; 23 - JUN - 1999; 23 - JUN - 1999; 24 - JUN - 1999; 26 - JUN - 1999; 27 - J
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29 - AUG - 1999;
27 - AUG - 1999;
       Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                       Zea mays DNA fragment SEQ ID NO: 31332.
                                                                                                                                                                                                                                                                                                                              990S-0121825P.
990S-0123148P.
990S-0125788P.
990S-0125788P.
990S-012624P.
990S-012624P.
990S-0128245P.
990S-0130610P.
990S-0130610P.
990S-0130640P.
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-MAY-1999;
-JUN-1999;
-JUN-1999;
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-JUN-1999;
-JUN-1999;
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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynuclectide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Prins radiata also known as Monteev pine). The protein sequences can be used to modify the response of plant cells to external signals. The polynuclectide and protein sequences can be used to modify the response of plant cells to external signals. C e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival resistance to disease and intered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers
                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.6%; Score 15.4; DB 3; Length 900; 94.1%; Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 149; 527pp; English.
                                                                                                                                                                                                                                   Strabala IJ, Nieuwenhuizen NJ;
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ADA71180/c
ID ADA71180 standard; DNA; 969 BP.
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Les 16, Conservative
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                        Eucalyptus grandis.
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01-NOV-1999;
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Pred. No. 1.9e+03;
0; Mismatches 1; Indels
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99US-0151080P.
99US-0151303P.
99US-015138P.
99US-0152363P.
99US-0153070P.
99US-0153078P.
99US-0154018P.
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990S-015645BP-
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99US-0161993P.
99US-0162142P.
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Local Similarity 94.1%;
les 16; Conservative
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15-SEP-1999;
16-SEP-1999;
                                                  01-SEP-1999
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28-SEP-19
29-SEP-19
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14-0CT-19
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25-0CT-1
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23-0CT-1
13-0CT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -0CT-1
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RESULT 5 AAA79481/c

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The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                          Hou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 969 BP; 196 A; 312 C; 309 G; 150 T; 0 U; 2 Other;
                                                                                          SA,
                                                                                          Goff.
                                                                                        Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID NO 4503; 899pp; English
                                                      (SYGN ) SYNGENTA PARTICIPATIONS AG
                22-JUN-2001; 2001WO-IB001105.
                                                                                          Cooper S, Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            illustrate the invention
                                                                                        Chen W, Co
?, Quan S,
                                                                                                                                              WPI; 2003-175290/17.
                                                                                                                                                                                                                                               gene expression.
                                                                                        Chang H, Ch
Katagiri F,
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Score 15.4; DB 7; Length 969; Pred. No. 1.8e+03; 0; Mismatches 1; Indels ( 2 GCGCCGGCGCAGGGGG 18 85.6%; ilarity 94.1%; Conservative Query Match Best Local Similarity Matches 16; Conserv 833 ઠે 셤

Eucalyptus grandis transcription factor DNA sequence #329. BD AACS6198 standard; DNA; 1008 (first entry) 25-JAN-2001 AACS6198; 

Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeodomain; homeocic; homeodomain; homeocic; homeodomain; nim domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.

Eucalyptus grandis. WO200053724-A2.

14-SEP-2000

09-MAR-2000; 2000WO-US006112.

99US-00266513. 99US-0149485P 11-MAR-1999; 18-AUG-1999;

FLETCHER CHALLENGE FORESTS LID. (GENE-) GENESIS RES & DEV CORP (FLET-) Glenn M; Shenk MA, Mcgrath A, Wood M,

WPI; 2000-579369/54

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide.

Claim 1; Page 131; 747pp; English

The present invention relates to novel plant transcription factors from bucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a mandgany species or to manylyptus, pine, acacia, poplar sweetgum, teak, or mandgany species or to madify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteims: bZIP, bZIP family of G-box hondmostic/homeodomain/homeobox/WALDS, homeofomain, zipper, LIM domain, AP2 and RREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and

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Sequence 1008 BP; 175 A; 315 C; 331 G; 187 T; 0 U; 0 Other;

Gaps . 0 Score 15.4; DB 3; Length 1008; Pred, No. 1.7e+03; 0; Mismatches 1; Indels 0; 85.6%; 94.1%; Query Match
Best Local Similarity 94.1'

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86 ABI99675 standard; cDNA; 1061 entry) (first 07-MAR-2002 AB199675; ø RESULT 

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Mouse ischaemic condition related cDNA sequence SEQ ID NO:711

Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;

Mus musculus.

WO200188188-A2.

22-NOV-2001

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977.

UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON,

Ishii Y; Nagata T, Takahashi Y, Asai S, Ishikawa K,

WPI; 2002-034733/04.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these

Claim 2; Page 1768-1769; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemia or oracition (e.g. compressive ischaemia, occlusive ischaemia or vasocspastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the

Sequence 1250 BP; 202 A; 407 C; 419 G; 222 T; 0 U; 0 Other;

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process sequences in ABB57020 to ABBS7374) or by determining the expression profile of a gene group comprising these genes. The expression lidicator expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels, as chromosome markers or tags, to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel coding seguence (useful for identifying genetic disorders) #481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; gene; ds.
                                                                                                                                                                                        Match 85.6%; Score 15.4; DB 6; Length 1061; Local Similarity 94.1%; Pred. No. 1.7e+03; les 16; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                     Sequence 1061 BP; 177 A; 284 C; 405 G; 191 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, bare Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Asundi V, Goodrich RW, Ren F,
Ghosh M, Kue AJ, Wehrman T, Weng G, 21
Ma Y. Wang D, Chen R, Ku C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 481; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               ADE07415 standard; DNA; 1250 BP
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14-MAR-2001; 2001US-0339453P.

14-MAR-2002; 2002US-036591P.

12-APR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-037815P.

22-APR-2002; 2002US-03786589.

24-APR-2002; 2002US-0376045P.
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The invention relates to an isolated nucleic acid comprising any one of the fall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid models a promoter operably linked to the nucleic acid conditions and promoter operably linked to the nucleic acid of the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding complypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an open product or that has an activity against a biological pathway cellurated for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological correction; (9) pathway in which a proliferation-required gene or its gene product lies correctly against a proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent compound's activity; (13) identifying the target of a compound that inhibits the
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Xu HH;
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or s. for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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drug design; gene.
   Length 1250;
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Yamamoto R, Forsyth RA,
Score 15.4; DB 9;
Pred. No. 1.7e+03;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                  Prokaryotic essential gene #24386.
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Carr GJ,
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06-6EP-2001, 2001US-0094893.
25-0CT-2001, 2001US-0342923P
08-FEB-2002, 2002US-0072851.
06-MAR-2002, 2002US-0362699P.
/ Match 85.6%;
Local Similarity 94.1%;
les 16; Conservative
                                                                                                                                                                                                      ACA42729 standard; DNA; 1404
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Trawick JD,
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Best Local S:
Matches 16
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Wang J; Wang Z;

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proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required dor cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, F. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antibarkinsonian; anticorvulsant; osteopathic; antiarthratic; antiinflammatory; dermatological; antiasthmatic; obesity; viral infection; bacterial infection; fungal infection; helminthic infection; protozoal infection; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; parkinson's disease; epilepsy; immune disorder; asthma; dyslipidemia; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grosse WM, Alsobrook JP, Anderson DW, Burgess CB, Edinger SR, Ellerman K, Furtak K, Gangolli EA, Gerlach VL, Gilbert JA, Gunther E, Gorman L, Guo K, Ji W, Li L, Miller CE, Padigaru M, Patturajan M, Rastelli L, Macdougall JR, Mishra VS, Smithson G; Spyrek KA, Stone DJ, Shenoy SG, Taupier RJ, Vernet CAM, Zhong M, Malyankar UM, Millet I, Kekuda R,
                                                                                                                                                                                                                                                       85.6%; Score 15.4; DB 7; Length 1404; 94.1%; Pred. No. 1.7e+03; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                    Sequence 1404 BP; 166 A; 458 C; 484 G; 296 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV9b coding sequence, SEQ ID 37.
                                                                                                                                                                                                                                                                                                                                                                        1154 receccececarece 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD49064 standard; DNA; 1611 BP
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15.JAN-2002; 2002US-0349182P.
17.JAN-2002; 2002US-0349182P.
18.JAN-2002; 2002US-034973F.
28.JAN-2002; 2002US-0351977P.
28.MAY-2002; 2002US-0381979P.
05.JUN-2002; 2002US-0387884P.
11.JUN-2002; 2002US-0387884P.
17.JUL-2002; 2002US-0387884P.
                                                                                                                                                                                                                                                                                                                                     1 TGCGCCGGCGCAGGGGG 17
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Best Local Similarity 94.1'
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003060149-A2.
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The present invention relates to novel NOV proteins and their coding sequences (ADD49028-ADD49131). The proteins and coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOV-associated disorder (viral, bacterial, fundal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), norexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), newrodegenerative disorders (osteoarthritis), hematopoietic disorders, inflammatory skin disorders, asthma and various dyslipidemias. The coding sequences and proteins may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell effect modules that modulate or inhibit e.g. neurogenesis, cell ifferentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind imunospecifically to NoV substances for use in therapeutic or diagnostic
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                                                                      New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Whitham S, Xie Z, Zhu T, Zou G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; DB 9; Length 1611; Pred. No. 1.7e+03; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1611 BP; 448 A; 403 C; 434 G; 326 T; 0 U; 0 Other;
                                                                                                                                                                 Claim 20; Page 144; 311pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GÓGGCGCCCAGGGGGG 132
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                             asthma, or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang H, Chen W, Co
Katagiri F, Quan S,
                   WPI; 2003-587288/55
P-PSDB; ADD49065.
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XXCCCCCCCCCCCCCCCXXXXCCCCCCCCCXXX
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                         Claim 6; SEQ ID NO 3209; 899pp; English.
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85.6%; Score 15.4; DB 7; Length 2196; 94.1%; Pred. No. 1.6e+03; ive 0; Mismatches 1; Indels 0 Sequence 2196 BP; 481 A; 542 C; 607 G; 563 T; 0 U; 3 Other; o; 7,8 Local Similarity 94.1 nes 16; Conservative Query Match Matches

356 dégeégéceckédégése 340 2 GCGCCGGCGCAGGGGGG ð g

ADD29815 standard; mRNA; 2448 15-JAN-2004 ADD29815; RESULT 13 

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(first entry)

Human tumour suppressor mRNA SEQ ID NO:311.

ss; human; tumour suppressor; cancer; cancer; cytostatic; gene therapy.

Homo sapiens

WO2003058201-A2.

17-JUL-2003

31-DEC-2002; 2002WO-US041825

31-DEC-2001; 2001US-0345317P

(QUAR-) QUARK BIOTECH INC. (CLEV-) CLEVELAND CLINIC FOUND.

Feinstein E, Gudkov AV;

WPI; 2003-598393/56.

Diagnosing cancer comprises determining the polypeptide or polymucleotide levels e.g., hepatic lipase, in a sample from a subject, where a higher level compared to that in a subject free of cancer is indicative of

Disclosure, SEQ ID NO 311, 272pp; English.

The invention relates to a novel method for diagnosing a cancer in a subject. the method comprises determining, in a sample from the subject, the level of at least one polypeptide, where a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer. The polypeptide is selected from any of specification and polypeptides which are at least 70% homologous to the polypeptides. The method of the invention has cytostatic activity, and markers specific for one or several types of cancer, depending on the tissue origin, which may be used in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic

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intervention. The compounds that modulate the activity of a tumour suppressor gene are useful in the treatment of cancer or as anti-cancer drugs. The present sequence represents a polynucleotide of the invention.
                                                                                                                                                                            Gaps
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                                                                                                                                  Length 2448;
                                                                                      Sequence 2448 BP; 573 A; 728 C; 609 G; 522 T; 0 U; 16 Other;
                                                                                                                                Query Match 85.6%; Score 15.4; DB 9; Length 2. Best Local Similarity 94.1%; Pred. No. 1.6e+03; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                490 GCGCCGCCCCGGGGG 506
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AAA79707 standard; cDNA; 2478 BP. (first entry) 27-NOV-2000 AAA79707; RESULT 14 AAA79707/c

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Gaps

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Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:859 Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival disease resistance; nutrient metabolism; ss.

Eucalyptus grandis.

WO200042171-A1

20-JUL-2000.

11-JAN-2000; 2000WO-US000724

99US-002289B6. 12-JAN-1999; 01-NOV-1999;

(GENE-) GENESIS RES & DEV CORP LTD.

Strabala TJ, Nieuwenhuizen NJ

WPI; 2000-476052/41.

Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals.

Claim 1; Page 415-416; 527pp; English.

AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in call signalling. The polynucleotide and protein sequences are involved in call signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripeding and sensoronce of leaves and flowers e.g. to delay sensoronce and prolong the life of cut flowers or enhance sensoronce of reproductive organs to engineer sterile plants. Other modifications can be used to delay sensoronce in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable Knot-free clear wood which can be used in solid timber furniture and veneers 

Sequence 2478 BP; 518 A; 756 C; 671 G; 533 T; 0 U; 0 Other;

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Score 15.4; DB 3; Length 2478; Pred. No. 1.6e+03; O; Mismatches 1; Indels 0;
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0
                                                                   2 GCGCCGGCGCAGGGGGG 18
Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative C
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243 GCGCCGGAGCAGGGGG 227

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RESULT 15 ADD15216 ID ADD1

ADD15216 standard; DNA; 2559 BP

ADD15216;

(first entry) 15-JAN-2004 Human serotonin 5-HT2 receptor DNA.

human; ds; mental disorder; differential gene expression; psychosis; schizophrenia; mood disorder; bipolar; major depression; neuroleptic; antidepressant; gene therapy.

Homo sapiens.

WO2003039490-A2

15-MAY-2003.

12-NOV-2002; 2002WO-US036683.

09-NOV-2001; 2001US-0339252P.

(UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFOR.

Evans S; Vawter MP; Bunney WE, Burke S, Choudary PV, Cox DR, Li J, Lopez JF, Myers RM, Thompson R, Akil H, B Watson SJ;

WPI; 2003-441464/41.

Determining a predisposition to mental disorders utilizing differential gene expression, useful for diagnosing, and/or treating mood disorders or psychosis, including bipolar and major depression disorders and schizophrenia.

Example 3; SEQ ID NO 24; 85pp; English.

This invention relates to a novel method for determining a predisposition to mental disorders by utilising differential gene expression.

Specifically, it refers to the differential gene expression of brain region specific nucleic acids that can be used to determine a prevalence of mental disorders with a gender bias. Accordingly, it comprises contacting a parients biological sample with a reagent (e.g. antibody) that selectively associates with a polymucleotide given in the specification, and detecting the level of reagent that associates to determine whether the subject has, or is predisposed for, a mental clistorder. As such, the present invention describes a method and disorders, such as psychosis e.g. schizophrenia or a mood disorder including bipolar and major depression disorders. These compositions have aforementioned conditions are the caforementioned conditions are the sequence is a brain specific gene (with gender bias) that is confer. used in an exemplification of the invention. 

Sequence 2559 BP; 579 A; 787 C; 627 G; 566 T; 0 U; 0 Other;

ö Gaps ·; Length 2559; 1; Indels Query Match 85.6%; Score 15.4; DB 9; Best Local Similarity 94.1%; Pred. No. 1.6e+03; Matches 16; Conservative 0; Mismatches 1;

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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

To Unpublished (197)

Contact: Robert Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (197)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Contact: Buck, M.D., Ph.D.

Conta Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
CC662082 OGVBNS8TH
CC3254827 OG1DX0TV
CC662091 OGVBNS8TV
CC662091 OGVBNS8TV
CC662091 OGVBNS8TV
CC6615817 OG1ADX15TV
CC255841 AGBNCOURT
CC255841 AGBNCOURT
CC255841 AGBNCOURT
CC25581 D601791154
BEC26629 L164-G88-BEC26625
AA613423 nG316.02-8
CE366192 L1GT-G88-BEC26625
AA613423 nG316.02-8
CE366192 L1GT-G88-BEC26626
AA613423 nG316.02-8
CE366192 L1GT-G88-BEC26626
AA613423 nG316.02-8
CE366192 L1GT-G88-BEC26626
CE36917 022-a01-r
CA483093 LA499495
BEC37116 WHE1821-1
BC811468 AA618499495
BEC37116 WHE1821-1
BC811468 AA618499495
BEC3716 CH20-404
AG145391 PPM LYCOG1
CC41502917 ETH1 41 B
BC3716 AC1820-404
AG145391 PPM LYCOG1
CC456433 COURAJESTH
BC671792 CG2643179 POLIL 12 F
BC766433 CG182165
BC7666433 CG182165
BC77792 GC2671135
AL204848 TELTACOGON
BFS31046 BC5017777
BC51266 BC5017777
BC51296 BC5017777
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320 bp mRNA linear EST 12-NOV-1997 nu99a09.s1 NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:1218808 3' similar to gb:X12794_cds1 V-ERBA RELATED PROTEIN BAR-2 (HUMAN);, AA662789
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PEATURES

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pBlueScript backbone); Site 1: BamHI; Site 2: BglII; Beschemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.rmdb.isstate.edu and follow the links for "RescueMu, Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and Bill, and ligated to form circular plasmids. DH10B ampicillin."
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1 (Dases 1 to 870)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
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Other_GSSs: OGIDX07TV
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: whitelaworigr.org
Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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/lab host="DH10B"
/clone_lib="NCI_CGAP_PT2"
/note="Organ: prostate; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker; lst strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Sto RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Patima Bonaldo. "
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases i to 565)
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Unpublished (2001)
Contact: Walbot V
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Stanford University
Stanford Uni
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/clone lib=="1008 - RescueMu Grid I"
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1008096D04.x1 1008 - RescueMu Grid I Zea mays genomic, genomic
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94.4%; Score 17; DB 9; L.
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 0;
                                                                   Trace considered overall poor quality
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
1. .320
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BH797911.1 GI:20307382
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CG254827 CG.7_1.5_KB Zea mays genomic clone ZMMBMa0740A14,
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Zea mays
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Eam mays
Entaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Entaryota, Viridiplantae, Streptophyta, Entaryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida, Poales;
Poaceae, PACCAD
Clade, Panicoideae, Andropogoneae, Zea.

1 (bases I to 929)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Gitek, R. W., Ruackenbush, J., Van Aken, S., Utterback, T.,
Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSS: CGlDX07TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
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methylation filtered genomic DNA library"
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llarity 100.0%; Pred. No. 5.7e+03;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR Medical Center Drive, Rockville, MD 20850, USA 712 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
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/strain="B73"
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Location/Qualifiers
  Seq primer: TR
Class: sheared ends.
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CG238619 B77 bp DNA linear GSS 22-AUG-2003 OG1AQ39TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0719G05, genomic survey sequence. CG238619. GI:34138505
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1 (Dases 1 to 907)
Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T., Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Ocher GSSs: OGVBNSBTV
Contact: Cathy Whitelaw
                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 877)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Rasnick, A., Praesr, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSS: OGIAQ397V
Contact: Cathy Whitelaw
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methylation filtered genomic DNA library"
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100.0%; Pred. No. 5.7e+03;
ive 0; Mismatches 0; Indels
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9712 Medical Center Drive, Rockville, MD 20850, USA
1913 101-898-5843
Fax: 301-838-6208
Email: whitelaw@tigr.org
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mass. 1 to 520)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagazi,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Massi,M.A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ307583
MRO-BT4507-220601-201-h03 BT4507 Homo sapiens CDNA, mRNA sequence.
BQ307583
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=hRO&t2=HRO-BT4507-
220601-201-h03&c3=2001-06-22&t4=1)
Seq primer: puc 18 forward
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/db ref="trans"| 2006"
/dev_stage="Adult"
/dov_stage="Adult"
/dove="Adult"
/clone lib="BT4567"
/note="Organ: breast, Vector: puc18; Site 1: Smal; Site 2: Smal, A mini-library was made by cloning products derived from Organsprep PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                              HincII; 0.7-1.5 kb
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                  94.4%; Score 17; DB 29; Length 972;
100.0%; Pred. No. 5.8e+03;
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Email: whitelaw@tigr.org
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                        Seq primer: TF
Class: sheared ends.
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                      CC662091

OGYBNSBTV ZM 0.7_1.5_KB Zea mays genomic clone ZMYBMa0496J20, genomic survey sequence.
CC62091.1 GI:32065976
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 964)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Clask, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Ocher GSS: OGUBNSETH
Contact: Cathy Whitelaw
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1 (bases 1 to 972)

Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Other GSSs: OGLAPISTH
Contact: Cathy Whitelaw
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methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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SOURCE ORGANISM

TITLE JOURNAL COMMENT

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Solanum tuberosum (potato)
Solanum tuberosum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                      Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1241
/organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
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1 TGCGCCGATGCAGGGGG 18
                                                                                                                                                          CD255841.1 GI:31016307
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                        임
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HHM1 and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5948
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                          CDAB3-C07.yld-s SHGC-CDA Gasterosteus aculeatus cDNA clone CDAB3-C07.yld-s sequence.
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                                                                                                                                                                                                                                                                                                      Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostcmi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Tercomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

1 (bases 1 to 1208)
1 (bases 1 to 208)
Schmutz, J. m., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, M..
Expressed sequence tags from Gasterosteus aculeatus
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\mathfrak{m}RNA and \mathfrak{cD}NA amplification were performed under low stringency conditions."
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                                                          Length
                                                                                     Indels
                                                         Score 16.4; DB 13;
Pred. No. 9.2e+03;
                                                         Query Match
91.1%; Score 16.4; Di
Best Local Similarity 94.4%; Pred. No. 9.2e
Matches 17; Conservative 0; Mismatches
                                                                                                                                  383 TGCGCCGCTGCAGGGGG 400
                                                                                                                 1 TGCGCCGATGCAGGGGG 18
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BST.
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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
I (bases 1 to 1241)
SI (hases 1 to 1241)
SI (hases 1 to 1241)
SI (hase 1 to 1241)
SI (hase 1 to 1241)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute (NIH)
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Gapba-remail.nih.gov
Tissue Procurement: ChNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLANIA578 row: j column: 09
High quality sequence stop: 384.
Ilocation/Qualifiers
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BST728765 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCAB91 3' end, mRNA sequence.
CD255841 11156934 NICHD_XGC_Brn1 Xenopus laevis CDNA clone IMAGE:6954538 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC_Brn1"
/clone_lib="NICHD XGC_Brn1"
/note="Organ brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size i.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library.
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Pred. No. 1.1e+04;
0; Mismatches 1; Indels 0;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilber Emith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: The I.M.A.G.B. Consortium

DNA Sequencing by: The I.M.A.G.B. Consortium

Clone distribution: NCT-CGAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LIML at:

thtp://image.libr.gov

http://image.libr.gov

laddity sequence stop: 584.

High quality sequence stop: 584.

Location/Qualifiers

/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF140016 595 bp mRNA linear EST 24-OCT-2000 601791154F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021788 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Rennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 595)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/cultivar="Kennebec"
/db xef="axon:4113"
/clone="PoCAB91"
/tissue type="callus"
/lab_bost="DHIOB-TonA"
/clone lib="pocate callus cDNA library, normalized and full-length"
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lammids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 322)
1 (bases 1 to 322)
1 (bases, Hart,A, Zismann,V., Karamycheva,S.A. and Baker,B. Generation of ESTs from potato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                    Unpublished (2003)
Other ESTS: EST728764
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Seq primer: GTA ATA CGA CTC ATA GGG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:10090"
/clone="IMAGE:4021788"
/tissue_type="tumor, metastatic to mammary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 322;
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                                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
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100.0%; Pred. No.
:ive 0; Mismatch
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/strain="Czech II"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musalia; Lucharia; Rodentia; Sciurognathi; Muridae; Murinae; Muss. Sarakar, C. (640); P., Fukuda, S., Furuno, M., Hanagaki, T., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, J., Nomura, K., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Sano, H., Sanaki, Y., Shibata, K., Saha, S., Sano, H., Sanaki, Y., Shibata, M., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tagami, M., Tagawa, A., Takahashi, F., Rikan Muses Ests (Arakawa, T., Muramatsu, M. and Hayashizaki, T., Rikan Muses Ests (Arakawa, T., et al. 2001)

Al Unpublished (2001)
Contact: Yoshihide Hayashizaki
Ishoratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Sciences Center(GSC), Yokohama Institute Sciences Center(GSC), Yokohama Institute Contact: Laboratory for Genome Exploration Tells Bl-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
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Email: genome-resegec riken.go.jp,

URL:http://genome-gec.riken.go.jp,

Carninol.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. . 10 (10), 1677-1630 (2000)

wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Matshura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.

and Hayashizaki,Y.

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sequencing pippline with 384 multicapillary sequencer. Genome Res.

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Konno,H., Pukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,

Sugaharaty. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Kondo,S., Shinagawa, S., Saito,T., Kiyosawa,H., Yamanaka,I.,

Alzawa,K., Pukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and

Hayashizaki,Y.

Alayashizaki,Y.

Alay
/lab_host="DH10B"

/cone lib="MCI_CGAP_Lu30"

/cone lib="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;

Site 2: Sall; transgenic model WNT-1, expression driven by

WMTV-LUR enhancer; Cloned unidirectionally. Primer: Oligo

dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB522625 RIKEN full-length enriched, 15 days embryo head Mus musculus cDNA clone D930008K19 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.4e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%; Sco.
100.0%; Pre
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Mus musculus
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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC In
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
072G16 of library G from Tetraodon nigroviridis, genomic survey
           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Taleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                /tissue_type="head"
/dev_stage="15_days_embryo"
/lab_host="DH108"
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Sauzin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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                                                                                                                                                             /organism="Mus musculus"
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/strain="C5/BL/6U"
/db_xref="taxon:10090"
/clone="D930008K19"
/sex="mixed"
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Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                     Location/Qualifiers
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further details.
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Submitted (12.APR.2000) Genoscope - Centre National de Sequencage : Submitted (12.APR.2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cms.fr. - Web : www.genoscope.cms.fr. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cms.fr/Tetraodon.
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                    compact genome of the
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/note="Genoscope sequence ID : COBG072BD08SP1~end
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Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the c
freshwater pufferfish Tetracodon ingroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                             1. .1063
/organism="Tetraodon nigroviridis"
/moltype="genomic DNA"
/db xref="taxon:99883"
/clone="072G16"
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Sequence 7939, Ap
Sequence 7799, Ap
Sequence 59, Appl
Sequence 1478, Ap
Sequence 16564, A
Sequence 6658, Ap
Sequence 6558, Ap
Sequence 6246, Ap
Sequence 6246, Ap
Sequence 6246, Ap
Sequence 6246, Ap
Sequence 42, Appl
Sequence 42, Appl
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Sequence 3473, Ap
Sequence 1229, Ap
Sequence 3666, Ap
Sequence 307, App
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16036, A
Sequence 45, Appl
Sequence 41, Appl
                                                                               2, 2004, 08:09:30 ; Search time 28.2073 Seconds (without alignments) 354.132 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-7999
US-09-252-991A-3760
US-09-489-039A-1478
US-09-252-991A-16564
US-09-620-312D-951
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US-09-318-448-4
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US-09-252-991A-3666
US-09-833-381-307
US-09-382-552-3
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Maximum Match 100%
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Sequence 7939, Application US/09252991A

Patent NO. 6551795
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 963
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Sequence 7799, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F.

TITLE OF INVENTION: AEMUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
US-09-182-552-117
US-09-182-552-115
US-09-182-552-15
US-09-182-552-14
US-09-182-552-14
US-09-182-552-14
US-09-182-552-17
US-09-182-552-19
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US-09-252-991A-16564/C

Sequence 16564, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REPERRICE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

WOMBER OF SEQ ID NOS: 33142

LENGTH: 885
                                                                                            RESULT 5
US-09-489-039A-1478
US-09-489-039A-1478
Sequence 1478, Application US/09489039A
Sett No. 6610836
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1478
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| Sequence 6558, Application US/09489039A
| Sequence 6558, Application US/09489039A
| Patent No. 6610836
| Patent No. 661086
| Patent No. 661086
| Patent No. 661086
| TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
| TITLE OF INVENTION: PRECMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 2709.2004001
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Pred. No. 6.1e+02;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 4; Length 885;
Pred. No. 6e+02;
0; Mismatches 2; Indels
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     124 TGCGCCGGCGCAGCGCG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-16564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Tececceacecaege 18
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AUCIELC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REPERENCE: 107156.136
CURRENT PEPLICATION NUMBER: US/09/252,991A
PRIOR PRILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER: US 60/094,190
PRIOR PILING DATE: 1999-07-27
NUMBER: US 60/094,190
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brown, Jr., Robert H.
APPLICANT: Brown, Jr., Robert H.
APPLICANT: Diu, Jing
APPLICANT: Liu, Jing
APPLICANT: Ho, Meng
APPLICANT: Ho, Meng
APPLICANT: Ho, Meng
APPLICANT: Ho, Meng
APPLICANT: Matsuda-Asada, Chie
TITLE OF INVENTION: USYSERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
TILL REFERENCE: 00786/399002
CURRENT APPLICATION NUMBER: US/09/382,552
CURRENT APPLICATION NUMBER: US/09/382,552
CURRENT APPLICATION NUMBER: US/09/382,552
BARLIER APPLICATION NUMBER: US/09/382,553
SAPLIER PILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: FastSEQ for Windows Version 3.0
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88.9%; Pred. No. 7e+02;
iive 0; Mismatches 2; Indels
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                                                                            Length 1050;
                                                         , DB 4; he...
0. 2e+02;
0; Indels
                                                                       Query Match 88.9%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 2e+Matches 16; Conservative 0; Mismatches
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2.09-252-991A-1760
; Sequence 3760, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                               8-09-382-552-59
Sequence 59, Application US/09382552
Patent No. 6673909
GENERAL INFORMATION:
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7799
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-09-382-552-59
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APPLICANT: MARC J.
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US-09-252-991A-16454/C

Sequence 16454, Application US/09252991A

Sequence 16454, Application US/09252991A

Faten No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLERC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQUENCE: 100 NO 16454
Sequence 6246, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY BRETON NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6246
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
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88.9%; Pred. No. 5.8e+02;
iive 0; Mismatches 2;
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Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
TITLE OF INVENTION: DEPELOPMENTAL DISORDERS
TITLE OF INVENTION: DEPELOPMENTAL DISORDERS
FILE REFREENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SSOFTMARE: PATENTIN VET. 2.0
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-16454
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
, ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6246
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Best Local Similarity 88.99
Matches 16; Conservative
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Best Local Similarity
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US-09-318-448-42
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                                                                                                                                                                                                                                                                                                              2; Indels
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APPLICANT: Mang, Dunuri
APPLICANT: Mang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 7846712B
GURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                               Score 14.8; DB 4;
Pred. No. 5.9e+02;
0; Mismatches 2;
  CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 1110
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PRIOR PILING DATE: 2000-04-25
PRIOR PPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 951
LENGTH: 1169
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                                                                                                                                                                                                                                                                                                                                                                                                     1031 rececercecenaeses 1014
                                                                                                                                                                   TYPE: DNA; CREbsiella pneumoniae; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6658
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Zhao, Qing A.
Wehrman, Tom
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Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
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Xue, Aidong J.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KBY: CDS
; LOCATION: (258)..(821)
US-09-620-312D-951
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                                                                                                                                                                                                                                                                  Query Match
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RESULT 9 US-09-489-039A-6246/c

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Sequence 13784, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION

GENERAL INFORMATION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                         APPLICANT: Johnson, william G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: 1059-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
LENGTH: 1275
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Pred. No. 5.8e+02;
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Pred. No. 5.7e+02;
0; Mismatches 2;
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                                                                                                                                                                       Sequence 41, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
                                                       261 Tácicicidecicecidedes 278
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ORGANISM: Pseudomonas aeruginosa
          1 TGCGCCGCCAGGGGG 18
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TYPE: DNA
) ORGANISM: Homo sapiens
US-09-318-448-41
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Best Local Similarity
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Job time: 29.2073 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-252-991A-13784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-13784
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 16036, Application US/09252991A

Batent No. 6551795

GENERAL INFORMATION:
APPLICANT: Narc J. Rubenfield et al.
TITLE OF INVENTION:
ARUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NGS: 33142
SEQ ID NO 16036
LENGTH: 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure

1 LOCATION: (290)

1 TOTHER INDEPARTION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-16036
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APPLICANT: Johnson, William G.
APPLICANT: Johnson, Edward S.
TITLE OF INVENTION: METHODS FOR DISORDERS
FILE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION WUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                       Score 14.8; DB 3; Length 1256;
Pred. No. 5.8e+02;
0; Mismatches 2; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 14.8; DB 4; Length 1269; 88.9%; Pred. No. 5.8e+02; ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.2%; Score 14.8; DB 3; Length 1273; Best Local Similarity 88.9%; Pred. No. 5.8e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0.
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Sequence 45, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION;
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                               Query Match 82.2%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                    ) TYPE: DNA
) ORGANISM: Homo sapiens
US-09-318-448-42
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CNGANISM: Homo sapiens
US-09-318-448-45
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LENGTH: 1256
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Gaps

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05; Search time 138.732 Seconds

(without alignments)

625.926 Million cell updates/sec
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Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

6326084

Post-processing: Minimum Match Maximum Match Listing first Listing first Listing first Database : Published Appl 1: /cgn2_6/pto 3: /cgn2_6/pto 4: /cgn2_6/pto 5: /cgn2_6/pto 6: /cgn2_6/pto 7: /cgn2_6/pto 7: /cgn2_6/pto 11: /cgn2_6/pto	100% 45 summaries 45 summaries 46 cata/2/pubpna/USO7 46ata/2/pubpna/USO6 46ata/2/pubpna/USO6 46ata/2/pubpna/USO6 46ata/2/pubpna/USO9
	18: /cgnz/procata/s/pubpia/ozi-unsw_tub:egq:* 18: /cgnz6/ptodata/z/pubpna/US60 NBW PUB.seq:* 19: /cgnz6/ptodata/z/pubpna/US60_PUBGOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 17, Appl	Seguence 5, Appli	Sequence 58926, A	Sequence 55777, A	Sequence 3377, Ap	Sequence 14407, A	Sequence 1956, Ap	Sequence 79096, A	Sequence 4446, Ap	Sequence 22077, A	Sequence 7873, Ap	Sequence 431, App	Sequence 99, Appl	Sequence 11115, A
	σI	US-10-068-160-17	US-10-666-022-5	US-10-437-963-58926	US-10-437-963-55777	US-10-437-963-3377	US-10-425-114-14407	US-10-198-846-1956	US-10-437-963-79096	US-10-029-386-4446	US-10-437-963-22077	US-10-198-846-7873	US-10-259-165-431	US-10-259-165-99	US-10-198-846-11115
		155	17	11	17	17	13	15	17	15	11	15	15	15	15
	Query Match Length DB	18	20	687	2052	369	483	513	573	597	616	664	681	684	745
عبن	Query Match	100.0	100.0	91.1	88.9	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85,6	85.6	85.6
	Score	18	18	16.4	16	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
	Result No.	-	7	ñ	Ω	υ N	φ υ	0	ω υ	о 0	10	Ω 11	c 12	c 13	c 14

equence 2950, A equence 41635, equence 94871, equence 21218, equence 282, Ap equence 282, Ap equence 21530, equ	72702, 29232, 24774, 100077, 30599, 16403,	3214 301 335 477 1029 1029	Sequence 102533, Sequence 67872, A Sequence 8591, App Sequence 95250, A Sequence 1132, Ap Sequence 1132, Ap Sequence 24, App1 Sequence 24, App1 Sequence 910, App
10-425-11 10-437-96 10-437-96 10-10-10-46	110-437-963- 110-425-114- 110-437-963- 110-282-1227- 110-425-114- 110-336-6034	-10-425-114-3214 -10-410-154-30 -10-369-493-3356 -10-085-198-47 -10-027-632-1025 -10-027-632-1025	US-10-027-633-102533 US-10-437-963-67872 US-10-437-963-69255 US-10-437-963-69250 US-10-437-963-69250 US-10-172-118-1132 US-10-293-582-24 US-10-437-963-34276 US-10-647-963-34276
13	1211121	113 114 113 113	100 100 100 100 100 100 100 100 100 100
785 804 807 900 929	951 1225 1344 1404 1486	1633 1728 1842 2071 2241 2241	2241 2329 2478 2478 2517 2559 2745 3104
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## ALIGNMENTS

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Sequence 17, Application US/10068160

Sequence 17, Application US/10068160

Sequence 17, Application US/10068160

Sequence 17, Application No. US2030066440A1

GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, Dennis
APPLICANT: SECRETARY, Dennis
APPLICANT: ISHIK, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
CURRENT PRILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin Version 3.1

SEQ ID NO 17

SEQ ID NO 17

SEQ ID NO 17

SER ORD NOS: 120

SOFTWARE: Patentin Version 3.1

SER OFFWARE: Patentin Version 3.1

SOFFWARE: Patentin Version 3.1

SER OFFWARE: Patentin Version 3.
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Db 1 TGGCCGGCGCAGGGG 18

RESULT 2 US-10-666-022-5 us-10-068-160-17.rnpb

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Sequence 3377, Application US/10437963
Sequence 3377, Application US/10437963
Sequence 3377, Application US/20040123343A1
GENERAL INFORMATION:
APPLICANT: Exou, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Backharov, Andrey A.
APPLICANT: Backharov, Bried Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUBER: US/10/437,963
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.9%; Score 16; DB 17; Length 2052; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_57751C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10359C.1
US-10-437-963-3377
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 55777
LENGTH: 2052
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                                                                   APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services APPLICANT: Kinman, Dennis M.
APPLICANT: Kinman, Dennis M.
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REPREDNCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT APPLICATION NUMBER: US 60/411,944
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR PILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SEQ ID NO SEQ ID NOS: 182
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Kovalica, Thomas J.
APPLICANT: La Kovalic, David K.
APPLICANT: La Kovalic, David K.
APPLICANT: Stou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Branch Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
LENGTH: 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 17; Length 20;
Pred. No. 1e+02;
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: LOCATION: (1)...(20)

: OTHER INFORMATION: n is a, c, g, or t, or no nucleotide

US-10-66-022-2
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US-10-437-963-58926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
  Sequence 5, Application US/10666022
Publication No. US20040105872A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 TGCGCCGCGCAGGGAG 187
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
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US-10-437-963-58926/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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RESULT

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Sequence 79096, Application US/10437963
Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: Exemple Thous J.
APPLICANT: Exemple Thous J.
APPLICANT: Cao, Yongwei
APPLICANT: Bouchartov, Andrey A.
APPLICANT: Buckhartov, Andrey A.
APPLICANT: Buckhartov, Andrey A.
APPLICANT: Buckhartov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Buckhartov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-029-386-4446/C
US-10-029-386-4446/C
Sequence 4446, Application US/10029386
Sequence 4446, Application US/10029386
Sequence 4446, Application US/20030194704A1
Sequence 4446, Application US/20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRENCE: ACOMICA-2
CURRENT APPLICATION WOMBER: US/10/029,386
CURRENT APPLICATION WOMBER: US/10/029,386
CURRENT APPLICATION WOMBER: US/10/029,386
CURRENT APPLICATION WOMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQUENCE Listing Engine vers. 1.1
SEQ ID NO 4446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 597;
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN PACKENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: SYNESPROT HIT: P34995, EVALUE 9.00e-16

OTHER INFORMATION: EST HUMAN HIT: A1953039.1, EVALUE 0.00e-10

US-10-029-386-4446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 17;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78839C.1
US-10-437-963-79096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Best Local Similarity 94.1%;
Matches 16; Conservative
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ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                    Sequence 14407, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Too, Vongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 32-21 (5313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 483
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ASSESSMENT, PREVENTION, AND
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US-10-19-846-1956/C

US-10-19-846-1956/Application US/10198846

Publication No US20030099974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Steinmann, Kathleen
APPLICANT: WOUZHON: NOVEL GENES, COMPOSITIONS, KIT:
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REPRENCE: WRI-049
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE FRAESQ for Windows Version 4.0

LENGTH: S13

LENGTH: S13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: LIB189-016-H8_FLI
US-10-425-114-14407
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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US-10-437-963-79096/c
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FEATURE:

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APPLICANT: Chang, Kun
APPLICANT: Chang, Hur-song
APPLICANT: Chang, Hur-song
APPLICANT: Chang, Hur-song
APPLICANT: Chang, Hur-song
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Kreps, Joel
APPLICANT: Moudhamer, Todal
APPLICANT: Moudhamer, Todal
APPLICANT: Moudhamer, Nicholas
APPLICANT: Micke, Darrell
APPLICANT: Micke, Darrell
APPLICANT: Micke, Darrell
APPLICANT: Wicke, Darrell
APPLIC
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APPLICANT: Glazebrock, Jane
APPLICANT: Katagiri, Pumiyaki
APPLICANT: Katagiri, Pumiyaki
APPLICANT: Koughamer, Todd
APPLICANT: Moughamer, Todd
APPLICANT: Ricke, Darzell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REPERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
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PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
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Publication No. US20030135888A1
GENERAL INFORMATION:
APPLICANT: Zhu, Tong
APPLICANT: Wang, Xun
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
                                                                                                                                                                                                               ; Sequence 431, Application US/10259165
; Publication No. US20030135888A1
295 GCGCGGCGCATGGGG 279
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US-10-259-165-431
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zhu, Tong
APPLICANT: Wang, Xu
                                                                                                                                            RESULT 12
US-10-259-165-431/c
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                                                                                     Sequence 22077, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bucknaruk, Brad
APPLICANT: Bucknaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 22077

LENGTH: 616
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; LOCATION: 16, 432, 474, 499, 500, 504, 516, 522, 523, 524, 531, 547,

; LOCATION: 548, 556, 558, 566, 567, 569, 578, 593, 594, 597, 612, 614,

; LOCATION: 620, 621, 628, 634, 637,

; OTHER INFORMATION: n = A,T,C or G
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ICATION, ASSESSMENT, PREVENTION, AND
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Pred. No. 5.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_27287C.1
US-10-437-963-22077
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Sequence 7873, Application US/10198846

Bublication No. US2030099974A1

GENERAL INFORMATION:

APPLICANT: Lillib., James

APPLICANT: Ku, YORDYAO

APPLICANT: Ku, YORDYAO

APPLICANT: Realmann, Kachleen

APPLICANT: Setimmann, Kachleen

TITLE OF INVENTION: POWIL GENES, COMPOSITIONS, K:

TITLE OF INVENTION: POWIL GENES, COMPOSITIONS, K:

TITLE OF INVENTION: POWIL GENES, COMPOSITIONS, K:

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SEQ ID NO 7873

LENGTH: 664
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-198-846-7873/c
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NUMBER OF SEQ ID NOS: 73128
                                 SEQ ID NO 2950
LENGTH: 785
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CENDICALION NO. US2004003488A1
CENDICALLION NO. US2004003488A1
CENDICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Uschie, David K
APPLICANT: Tabaska, Uschie, David K
APPLICANT: Core, Yongwin
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: UNMERR: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
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PUblication No. US20030099974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Mange, Yourn
TITLE OF INVENTION: Rathleen
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: 2002-07-18

FILE REFERENCE: MRI-049

CURRENT PELICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2001-07-18

NUMBER: OF SEQ ID NOS: 14084

NUMBER: OF SEQ ID NOS: 14084

SOFTWARE: Faster of Faster of Mindows Version 4.0
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                                                                                                                                                                                                                                                              Query Match 85.6%; Score 15.4; DB 15; Length 684; Best Local Similarity 94.1%; Pred. No. 5.4e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0.
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85.6%; Score 15.4; DB 15; Length 745;

Best Local Similarity 94.1%; Pred. No. 5.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 99
LENGTH: 684
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                           1 TGCGCCGGCGCAGGGGG 17
                                                                                                                                                         TYPE: DNA
CORGANISM: Oryza sativa
US-10-259-165-99
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-198-846-11115
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LENGTH: 745
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| SEQ IN NO 2950
| TYPE: DNA |
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